



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 153564

**TO: Minh-Tam Davis**  
**Location: REM/3A24/3C18**  
**Art Unit: 1642**  
**Friday, May 20, 2005**

**Case Serial Number: 09/976858**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**Remsen 1-A-62**  
**Phone: 571-272-2524**

**[maryjane.ruhl@uspto.gov](mailto:maryjane.ruhl@uspto.gov)**

### Search Notes

Examiner Davis,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524



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From: Chan, Christina  
Sent: Monday, May 16, 2005 4:39 PM  
To: Davis, Minh-Tam; STIC-Biotech/ChemLib  
Subject: RE: Rush search request for 09/976858

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Monday, May 16, 2005 3:53 PM  
To: Chan, Christina  
Subject: Rush search request for 09/976858

Please search in commercial database, issued patent files, PGPUB and interference:

- 1) SEQ ID NO:41
- 2) oligomer search for SEQ ID NO:41, with size limitation for the sequences in the database less than 500 nucleotides.

Please have the search results in both paper and disk.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18  
272-0830

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 16:18:52 ; Search time 1981 Seconds  
(without alignments)  
11887.295 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcccgtgtaccagga.....ttttcgagacgactgtga 3978

Scoring table: OLIGO\_NUC

Gapop\_60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6273088

Minimum DB seq length: 0

Maximum DB seq length: 500

Post-processing: Listing first 45 summaries

Database: N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366	9.2	486	2 AAT94053	Aat94053 Partial h
C 2	336	8.4	424	5 ABV40627	Abv40627 Human pro
C 3	308	7.7	407	5 ABV40332	Abv40332 Human pro
4	283	7.1	442	5 ABV24239	Abv24239 Human pro
5	252	6.3	425	5 ABV41910	Abv41910 Human pro
6	216	5.4	291	4 AAH93897	Aah93897 P510S-C c
7	216	5.4	291	4 AAS64133	Aas64133 Human CDN
8	216	5.4	291	5 ACA59941	Aca59941 Prostate
9	216	5.4	291	6 ABL95504	Ab195504 P510S-C c
10	216	5.4	291	8 ACC95668	Acc95668 Prostate
11	216	5.4	291	10 ADB14273	Adb14273 Human pro
12	216	5.4	291	10 ADG26689	Adg26689 Human pro
13	211	5.3	439	2 AAX40493	Aax40493 Human sec
14	210	5.3	391	5 ABV41670	Abv41670 Human pro
15	208	5.2	444	5 ABV32629	Abv32629 Human pro
16	208	5.2	482	5 ABV11484	Abv11484 Human pro
17	196	4.9	456	5 ABV21425	Abv21425 Human pro
18	196	4.9	456	5 ABV27243	Abv27243 Human pro
C 19	176	4.4	345	5 ABV10192	Abv10192 Human pro
C 20	176	4.4	412	5 ABV31363	Abv31363 Human pro

C	21	145	3.6	273	5	ABV38375	Abv38375 Human pro
	22	142	3.6	329	5	ABV32745	Abv32745 Human pro
	23	142	3.6	416	5	ABV11600	Abv11600 Human pro
C	24	141	3.5	409	5	ABV11417	Abv11417 Human pro
C	25	141	3.5	433	5	ABV41487	Abv41487 Human pro
C	26	141	3.5	433	5	ABV32562	Abv32562 Human pro
	27	138	3.5	469	5	ABV27424	Abv27424 Human pro
	28	138	3.5	469	5	ABV21605	Abv21605 Human pro
	29	138	3.5	469	5	ABV20845	Abv20845 Human pro
	30	137	3.4	350	5	ABV13007	Abv13007 Human pro
	31	137	3.4	425	5	ABV03838	Abv03838 Human pro
C	32	136	3.4	462	5	ABV02188	Abv02188 Human pro
C	33	136	3.4	484	5	ABV11357	Abv11357 Human pro
C	34	133	3.3	372	5	ABV02248	Abv02248 Human pro
	35	132	3.3	403	5	ABV11840	Abv11840 Human pro
	36	132	3.3	422	5	ABV32985	Abv32985 Human pro
	37	127	3.2	391	5	ABV06629	Abv06629 Human pro
C	38	125	3.1	439	5	ABV36508	Abv36508 Human pro
	39	114	2.9	281	5	ABV36609	Abv36609 Human pro
	40	111	2.8	432	5	ABV37059	Abv37059 Human pro
	41	110	2.8	339	5	ABV36578	Abv36578 Human pro
	42	105	2.6	220	5	ABV06661	Abv06661 Human pro
	43	98	2.5	377	12	ADH10618	Adh10618 Human can
	44	93	2.3	387	5	ABV02315	Abv02315 Human pro
C	45	91	2.3	363	5	ABV06557	Abv06557 Human pro

#### ALIGNMENTS

##### RESULT 1

AAT94053

ID AAT94053 standard; cDNA; 486 BP.

XX AAT94053;

XX 25-MAR-2003 (revised)

DT 01-APR-1998 (first entry)

XX Partial human multidrug resistance-associated protein 4 (hMRP4) cDNA.

XX Canalicular multispecific organic anion transporter protein;

KW cMOAT protein; ATP-binding cassette transporter family; ABC transporter;

KW hepatobiliary excretion; multidrug resistance-associated protein; MRP4;

KW cMOAT protein activity; multidrug resistance-related protein; MDR-1;

KW Dubin-Johnson disease; Rotor disease; ss.

XX Homo sapiens.

XX WO9731111-A2.

PN 28-AUG-1997.

XX 21-FEB-1997; 97WO-NL000079.

XX 22-FEB-1996; 96EP-00200460.

XX (INTR-) INTROGENE BV.

PA (MEDI-) ACAD MEDISCH CENT AMSTERDAM.

PA (HETN-) HET NEDERLANDS KANKER INST.

PI Oude Elferink RPJ, Paulusma CC, Bosma PJ, Borst P, Evers R;

PI Kool M;

XX WPI; 1997-435163/40.

XX DNA encoding human and rat canalicular multispecific organic anion

PT transporter proteins - useful for diagnosis and treatment of Dubin-

PT Johnson disease and Rotor disease.

XX Disclosure; Fig 18; 106pp; English.

XX The present cDNA sequence encodes a partial human multidrug resistance-



DT 16-SEP-2002 (first entry)  
 XX Human prostate expression marker cDNA 40323.  
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 OS Homo sapiens.  
 XX WO200160860-A2.  
 XX 23-AUG-2001.  
 XX 20-FEB-2001; 2001WO-US005171.  
 XX 17-FEB-2000; 2000US-0183319P.  
 XX 16-MAR-2000; 2000US-0189862P.  
 XX 25-MAY-2000; 2000US-0207454P.  
 XX 09-JUN-2000; 2000US-0211314P.  
 XX 18-JUL-2000; 2000US-0219007P.  
 XX 13-DEC-2000; 2000US-0255281P.  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX Schlegel R, Endege WO, Monahan JE;  
 XX WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX Claim 1; Page 8142; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 407 BP; 108 A; 96 C; 97 G; 106 T; 0 U; 0 Other;  
 Query Match 7.7%; Score 308; DB 5; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-142;  
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1955 GTACCTTCTCAGAGTCTTCGGTTGGTCTCAACAATCTTCAGACCTCTTGAAGATG 2014  
 Db 374 GTACCTTCTCAGAGTCTTCGGTTGGTCTCAACAATCTTCAGACCTCTTGAAGATG 315  
 Qy 2015 GTGCTCTGGAGCCAGATACAGAGATGTCAGATGTCAGATGTCAGAGGAGACCGTT 2074  
 Db 314 GTGCTCTGGAGCCAGATACAGAGATGTCAGATGTCAGATGTCAGAGGAGACCGTT 255  
 Qy 2075 CTGAAGGAAAATGTTGGTTTTCAGGCTTAAGAATTAATCTCAGAGCTGGTCTCACTGGA 2134  
 Db 254 CTGAAGGAAAATGTTGGTTTTCAGGCTTAAGAATTAATCTCAGAGCTGGTCTCACTGGA 195  
 Qy 2135 TTGCTTCAATTTCTTATTTCTTAAACACTGAGCTCAGGTGCTTCAAGTCTTCAAG 2194  
 Db 194 TTGCTTCAATTTCTTATTTCTTAAACACTGAGCTCAGGTGCTTCAAGTCTTCAAG 135  
 Qy 2195 ATTGGTGGCTTTTCACTTGGGCAACAAACAAAGATGCTAAATGCTCACTTAATGGAG 2254  
 Db 134 ATTGGTGGCTTTTCACTTGGGCAACAAACAAAGATGCTAAATGCTCACTTAATGGAG 75

Qy 2255 GAGGAAAT 2262  
 Db 74 GAGGAAAT 67  
 RESULT 4  
 ABV24239  
 ID ABV24239 standard; cDNA; 442 BP.  
 XX AC ABV24239;  
 XX 16-SEP-2002 (first entry)  
 XX Human prostate expression marker cDNA 24230.  
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX Homo sapiens.  
 XX WO200160860-A2.  
 XX 23-AUG-2001.  
 XX 20-FEB-2001; 2001WO-US005171.  
 XX 17-FEB-2000; 2000US-0183319P.  
 XX 16-MAR-2000; 2000US-0189862P.  
 XX 25-MAY-2000; 2000US-0207454P.  
 XX 09-JUN-2000; 2000US-0211314P.  
 XX 18-JUL-2000; 2000US-0219007P.  
 XX 13-DEC-2000; 2000US-0255281P.  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX Schlegel R, Endege WO, Monahan JE;  
 XX WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX Claim 1; Page 4528; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 442 BP; 121 A; 91 C; 110 G; 120 T; 0 U; 0 Other;  
 Query Match 7.1%; Score 283; DB 5; Length 442;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-130;  
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 532 GCATTTGCTTTAGTAATGCGCCATGGGGAAGAACACACAGCCAGATGTAATCTG 591  
 Db 109 GCATTTGCTTTAGTAATGCGCCATGGGGAAGAACACACAGCCAGATGTAATCTG 168  
 Qy 592 CTGTCCAAATGATGTAACAGTTTGTATCAGTGACAGTGTTCTTACACTTCTGTGGGCA 651  
 Db 169 CTGTCCAAATGATGTAACAGTTTGTATCAGTGACAGTGTTCTTACACTTCTGTGGGCA 228  
 Qy 652 GGACCACTGCGGCGATCGGAGTGAATGCTGCTGAGATGAGATAGTAATGCTGTC 711

Db 229 GGACCACTGGGGGATCGAGTGAATGCTTCTGGATGGAGATAGGATATCGTGC 288  
Qy 712 CTGCTGGGATGGCAGTTCTAATCATCTCTGCGCCCTTGGCAAGCTGTTTGGGAAGTTG 771  
Db 289 CTGCTGGGATGGCAGTTCTAATCATCTCTGCGCCCTTGGCAAGCTGTTTGGGAAGTTG 348  
Qy 772 TTCTCATCACTGAGGAGTAAACTGCACTTTTCAGGATGCCAGATCAGACCATGAT 831  
Db 349 TTCTCATCACTGAGGAGTAAACTGCACTTTTCAGGATGCCAGATCAGACCATGAT 408  
Qy 832 GAAAGTTAATCTGGTATAGGATATATAAATGT 865  
Db 409 GAAAGTTAATCTGGTATAGGATATATAAATGT 442

## RESULT 5

ID ABV41910 standard; cDNA; 425 BP.

XX AC ABV41910;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 41901.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of  
XX PT prostate cells and correlating with presence of prostate cancer, useful  
XX PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 8407-8408; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising  
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
XX CC specification or its complement. (I) is useful for: (a) assessing whether  
XX CC a patient is afflicted with prostate cancer; (b) monitoring the  
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy  
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
XX CC determining whether prostate cancer has metastasized in a patient; (h)  
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient  
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

SQ Sequence 425 BP; 108 A; 91 C; 102 G; 124 T; 0 U; 0 Other;

Query Match

Best Local Similarity 6.3%; Score 252; DB 5; Length 425;

100.0%; Pred. No. 1.2e-114;

Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 532 GCATTCGTCTTAGTAACATGGCCATGGGAAGCAACCAAGCAGATAGTCAATCTG 591  
Db 174 GCATTCGTCTTAGTAACATGGCCATGGGAAGCAACCAAGCAGATAGTCAATCTG 233  
Qy 592 CTGTCCAATGATGTGAACAAGTTTGTGATCAGTGACAGTGTCTTACACTTCTCTGGGCA 651  
Db 234 CTGTCCAATGATGTGAACAAGTTTGTGATCAGTGACAGTGTCTTACACTTCTCTGGGCA 293  
Qy 652 GGACCACTGCAGGCGATCGCAGTGAATCTCTGGATGGAGATAGGAATATCGTGC 711  
Db 294 GGACCACTGCAGGCGATCGCAGTGAATCTCTGGATGGAGATAGGAATATCGTGC 353  
Qy 712 CTGCTGGGATGGCAGTTCTAATCATCTCTGCGCCCTTGGCAAGCTGTTTGGGAAGTTG 771  
Db 354 CTGCTGGGATGGCAGTTCTAATCATCTCTGCGCCCTTGGCAAGCTGTTTGGGAAGTTG 413  
Qy 772 TTCTCATCACTG 783  
Db 414 TTCTCATCACTG 425

## RESULT 6

ID AAH93897 standard; cDNA; 291 BP.

XX AC AAH93897;

XX DT 04-OCT-2001 (first entry)

XX DE PS10S-C construct cDNA sequence.

XX KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
XX KW cytostatic; gene therapy; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200151633-A2.

XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001574.

XX PR 14-JAN-2000; 2000US-00483672.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
XX PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;  
XX PI Wang A, Meagher MJ;

XX DR WPI; 2001-425873/45.

XX PT New polynucleotide encoding a prostate-specific protein, for diagnosing,  
XX PT monitoring and treating prostate cancer in a patient and for use in  
XX PT vaccines.

XX PS Claim 1; Page 493; 543pp; English.

XX CC The present invention describes polynucleotide sequences (I) which encode  
XX CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
XX CC and can be used in vaccine production and gene therapy. (I), (II),  
XX CC antibodies to (II), fusion proteins comprising (II), and isolated T cells  
XX CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and  
XX CC the antibodies are also used in the detection of cancer in a patient. The  
XX CC cancer that is diagnosed or treated is particularly prostate cancer. (I)  
XX CC and (II) can be used in vaccines. The antibodies or (I) can be used for  
XX CC monitoring the progression of cancer in a patient. (I) and (II) can also  
XX CC be used to improve diagnostic and therapeutic methods for prostate  
XX CC cancer. They can indicate the level of metastasis as well as the prostate  
XX CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent  
XX CC polynucleotide and amino acid sequences used in the exemplification of



PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;  
PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;  
XX  
DR WPI; 2001-245062/25.  
XX  
XX Prostate specific protein and its encoding polynucleotide, useful for the  
PT treatment and diagnosis of prostate cancer.  
PT  
PS Disclosure; SEQ ID NO 823; 85pp; English.  
XX  
CC The invention describes a fusion protein comprising at least one amino  
CC acid sequence of immunogenic portions of any of the 3 sequences not  
CC defined in the specification, or sequences having at least 70 or 90 %  
CC sequence identity to any one of the 35 sequences defined in the USPTO web  
CC site, which is encoded by any of the 4 nucleotide sequences not defined  
CC in the specification. The fusion protein, composition and methods are  
CC useful for diagnosing, preventing and/or treating cancer, particularly  
CC prostate cancer. The proteins are useful as markers to indicate the  
CC presence or absence of cancer. This sequence represents a prostate cancer  
CC therapy associated cDNA. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from the US patent office at  
CC seqdata.uspto.gov/sequence.html?docID=US20020192763  
XX  
SQ Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;

Query Match 5.4%; Score 216; DB 5; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCATTCACACAGATTGAACACCAT 3714  
Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCATTCACACAGATTGAACACCAT 66

Qy 3715 ATTGACAGCGACAAGATATGGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCG 3774  
Db 67 ATTGACAGCGACAAGATATGGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCG 126

Qy 3775 TATGTTTTCGCAAAATTAAGAGAGCCCTATTTTACAGATGGTGCAACACTGGGAAG 3834  
Db 127 TATGTTTTCGCAAAATTAAGAGAGCCCTATTTTACAGATGGTGCAACACTGGGAAG 186

Qy 3835 GCAGAGCGCGTGCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAGCGCGTGCCTCACTGAAACAGCAAAACAG 222

RESULT 9  
ID ABL95504  
XX ABL95504 standard; cDNA; 291 BP.  
AC ABL95504;  
XX  
XX 29-AUG-2003 (revised)  
DT 19-JUL-2002 (first entry)  
XX  
DE P510S-C construct cDNA sequence SEQ ID NO 823.

XX  
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;  
KW gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
OS Chimeric.  
XX  
PN US2002022248-A1.  
XX  
PD 21-FEB-2002.  
XX  
XX 12-JAN-2001; 2001US-00759143.  
XX  
PR 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 10-FEB-1998; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
PR 14-JUL-1998; 98US-00115453.  
PR 23-SEP-1998; 98US-00159812.  
PR 15-JAN-1999; 99US-00232149.  
PR 09-APR-1999; 99US-00288946.  
PR 13-JUL-1999; 99US-00352616.  
PR 12-NOV-1999; 99US-00439313.  
PR 18-NOV-1999; 99US-00443686.  
PR 14-JAN-2000; 2000US-00483672.  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PR 12-MAY-2000; 2000US-00570737.  
PR 13-JUN-2000; 2000US-00593793.  
PR 27-JUN-2000; 2000US-00605783.  
PR 10-AUG-2000; 2000US-00636215.  
PR 29-AUG-2000; 2000US-00651236.  
PR 08-SEP-2000; 2000US-00657279.  
PR 02-OCT-2000; 2000US-00679426.  
PR 10-OCT-2000; 2000US-00685166.  
XX  
XX (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
XX  
XX WPI; 2002-255649/30.  
XX  
XX New prostate-specific polynucleotides for diagnosing and treating  
PT diseases, in particular prostate cancer, and as markers for the  
PT progression of cancer.  
XX  
XX Claim 1; SEQ ID NO 823; 87pp; English.  
XX  
CC The present invention provides prostate-specific coding sequences and  
CC their encoded proteins. These can be used in the diagnosis and treatment  
CC of cancers, particularly prostate cancer. The present sequence is a cDNA  
CC described in the invention. (Updated on 29-AUG-2003 to standardise OS  
XX field)  
XX  
SQ Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;

Query Match		5.4%; Score 216; DB 6; Length 291;
Best Local Similarity		100.0%; Pred. No. 1.le-96;
Matches 216; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
Qy	3555	ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714
Db	7	ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66
Qy	3715	ATTGACAGCGACAAGATAATGTTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCG 3774
Db	67	ATTGACAGCGACAAGATAATGTTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCG 126
Qy	3775	TATGTTTTGCTGCAAAATAAAGAGAGAGCCTATTTTACAAGATGGTGCACAACTGGGCAAG 3834
Db	127	TATGTTTTGCTGCAAAATAAAGAGAGAGCCTATTTTACAAGATGGTGCACAACTGGGCAAG 186
Qy	3835	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db	187	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 222
RESULT 11		
ADBI4273		
ID	ADBI4273	standard; cDNA; 291 BP.
XX	XX	
AC	ADBI4273;	
XX	XX	
DT	18-DEC-2003	(first entry)
XX	XX	
DE	Human prostate specific protein P510S-construct C cDNA.	
KW	Human; ss; prostate specific cDNA; cytostatic; immunostimulant;	
KW	gene therapy; cell therapy; vaccine; T-cell epitope;	
KW	class I major histocompatibility complex allele; MHC; prostate cancer;	
KW	tumour; antigen presenting cell; gene; fusion protein.	
OS	Homo sapiens.	
XX	XX	
PN	US2003185830-A1.	
XX	XX	
PD	02-OCT-2003.	
XX	XX	
PF	12-NOV-2002; 2002US-00294025.	
XX	XX	
PR	25-FEB-1997; 97US-00806099.	
PR	01-AUG-1997; 97US-00904804.	
PR	09-FEB-1998; 98US-00020956.	
PR	25-FEB-1998; 98US-00030607.	
PR	14-JUL-1998; 98US-00115453.	
PR	23-SEP-1998; 98US-00159812.	
PR	15-JAN-1999; 99US-00232149.	
PR	09-APR-1999; 99US-00288946.	
PR	13-JUL-1999; 99US-00352616.	
PR	12-NOV-1999; 99US-00439313.	
PR	18-NOV-1999; 99US-00443686.	
PR	14-JAN-2000; 2000US-00483672.	
PR	27-MAR-2000; 2000US-00536857.	
PR	09-MAY-2000; 2000US-00568100.	
PR	12-MAY-2000; 2000US-00570737.	
PR	13-JUN-2000; 2000US-00593793.	
PR	27-JUN-2000; 2000US-00605783.	
PR	09-AUG-2000; 2000US-00636215.	
PR	29-AUG-2000; 2000US-00651236.	
PR	06-SEP-2000; 2000US-00657279.	
PR	02-OCT-2000; 2000US-00679426.	
PR	10-OCT-2000; 2000US-00685166.	
PR	09-NOV-2000; 2000US-00709729.	
PR	12-JAN-2001; 2001US-00759143.	
PR	09-FEB-2001; 2001US-00780669.	
PR	09-MAY-2001; 2001US-00852911.	
PR	29-JUN-2001; 2001US-00895814.	
PR	10-DEC-2001; 2001US-00012896.	
PR	09-MAY-2002; 2002US-00144678.	
RESULT 10		
ACC95668		
ID	ACC95668	standard; cDNA; 291 BP.
XX	XX	
AC	ACC95668;	
XX	XX	
DT	28-AUG-2003	(first entry)
XX	XX	
DE	Prostate tumour specific cDNA sequence SEQ ID 823.	
KW	Cytostatic; gene therapy; prostate-specific protein; PSP; human;	
KW	immune response; prostate cancer; ss.	
OS	Homo sapiens.	
XX	XX	
PN	WO200289747-A2.	
XX	XX	
PD	14-NOV-2002.	
XX	XX	
PF	09-MAY-2002; 2002WO-US014753.	
XX	XX	
PR	09-MAY-2001; 2001US-00852911.	
PR	29-JUN-2001; 2001US-00895814.	
PR	10-DEC-2001; 2001US-00012896.	
XX	XX	
PA	(CORI-) CORIXA CORP.	
XX	XX	
PI	Xu J, Dillion DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;	
PI	Kalos MD, Ranger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;	
PI	Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;	
PI	McNeill PD, Houghton RL, Vinals Y De Bassolac, Foy TM, Watanabe Y;	
PI	Deng T;	
XX	XX	
DR	WPI; 2003-167130/16.	
XX	XX	
PT	New prostate-specific proteins and genes, useful in gene therapy,	
PT	particularly for stimulating an immune response in a patient, or treating	
PT	prostate cancer in a patient, as well as for diagnosing prostate cancer	
PT	in a patient.	
XX	XX	
XX	Example 17; Page 602; 691pp; English.	
XX	XX	
CC	The present invention relates to novel prostate-specific proteins (PSP)	
CC	and their coding sequences. The PSPs and their coding sequences are	
CC	useful for stimulating an immune response in a patient, or for treating	
CC	prostate cancer in a patient and for determining, detecting or diagnosing	
CC	the presence of a cancer in a patient. The present sequence was used to	
CC	illustrate the invention	
XX	XX	
SQ	Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;	

XX PA (CORI-) CORIXA CORP.  
 XX PI Xu J, Stolk JA, Kalos MD;  
 XX DR WPI; 2003-756193/71.  
 XX DR P-PSDB; ADB14276.  
 XX  
 PT New isolated polypeptide for use in a vaccine for stimulating an immune  
 PT response, or for treating or diagnosis cancer, preferably prostate  
 PT cancer.  
 XX  
 PS Example 17; Page; 101pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide comprising no more than  
 CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The  
 CC peptides comprise a fragment ADB13563 of that contain naturally processed  
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)  
 CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific  
 CC cDNA, one of 648 disclosed as new. Also included are nucleic acids  
 CC encoding the proteins and peptides, expression vectors, a host cell  
 CC transformed with the vector, an isolated antibody (or antigen binding  
 CC fragment) that specifically binds to the protein or peptide, detecting  
 CC the presence of a cancer in a patient (comprising contacting a patient  
 CC sample with a binding agent that binds to the peptides or a polypeptide  
 CC appearing as ADB1358, detecting the amount of polypeptide that binds to  
 CC the agent and comparing the amount of polypeptide to a predetermined cut-  
 CC off value to determine the presence of cancer), a fusion protein  
 CC comprising the peptides or proteins, stimulating or expanding T cells  
 CC specific for a tumour protein comprising contacting T cells with the  
 CC peptides or the isolated T cell population, treating prostate cancer in a  
 CC patient comprising administering a composition comprising the peptides,  
 CC nucleic acids, antibodies or compounds, determining the presence of a  
 CC cancer in a patient and treating prostate cancer in a patient comprising  
 CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated  
 CC from a patient with the peptides or antigen presenting cells that express  
 CC the peptides so that the T cells proliferate, and administering the  
 CC proliferated T cells to the patient. The peptides (or an oligonucleotide  
 CC that hybridises to nucleic acid encoding them), is used to detect the  
 CC presence of cancer in a patient. The peptides, nucleic acids encoding, or  
 CC antigen-presenting cells expressing the nucleic acid, are used to  
 CC stimulate or expand T cells specific for a tumour protein. The peptides,  
 CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen  
 CC presenting cells are used to stimulate an immune response or treat  
 CC prostate cancer in a patient. The present sequence is a cDNA encoding a  
 CC fusion protein comprising a prostate specific protein. Note: Except where  
 CC otherwise indicated, the sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.  
 XX  
 SQ Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
 Query Match 5.4%; Score 216; DB 10; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 1.le-96;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3655 ATCCGGGAGAAATTTGCCACTGCACCGTGTACCATTTGCACACAGATTTGACACCATTT 3714  
 Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTACCATTTGCACACAGATTTGACACCATTT 66  
 Qy 3715 ATTCACAGCGACAGATTAATGTTTATGATTTCAGAGACTGAAGATATGATGAGCG 3774  
 Db 67 ATTCACAGCGACAGATTAATGTTTATGATTTCAGAGACTGAAGATATGATGAGCG 126  
 Qy 3775 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAGATGTTGCAACAACTGGGCAAG 3834  
 Db 127 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAGATGTTGCAACAACTGGGCAAG 186  
 Qy 3835 GCAGAGCGCGTGCCTCCTCAGTGAACAGCAAAACAG 3870  
 Db 187 GCAGAGCGCGTGCCTCCTCAGTGAACAGCAAAACAG 222

RESULT 12  
 ADG26689  
 ID ADG26689 standard; cDNA; 291 BP.  
 XX  
 AC ADG26689;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human prostate-specific cDNA #665.  
 XX  
 KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;  
 KW cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2003157089-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PP 09-MAY-2002; 2002US-00144678.  
 XX  
 PR 25-FEB-1997; 97US-00806099.  
 PR 01-AUG-1997; 97US-00904804.  
 PR 09-FEB-1998; 98US-00020956.  
 PR 25-FEB-1998; 98US-00030607.  
 PR 14-JUL-1998; 98US-00115453.  
 PR 23-SEP-1998; 98US-00159812.  
 PR 15-JAN-1999; 99US-00232149.  
 PR 09-APR-1999; 99US-00288946.  
 PR 13-JUL-1999; 99US-0032616.  
 PR 12-NOV-1999; 99US-00439313.  
 PR 18-NOV-1999; 99US-00443686.  
 PR 14-JAN-2000; 2000US-00483672.  
 PR 27-MAR-2000; 2000US-00536857.  
 PR 09-MAY-2000; 2000US-00568100.  
 PR 13-JUN-2000; 2000US-00570737.  
 PR 27-JUN-2000; 2000US-00593793.  
 PR 09-AUG-2000; 2000US-00605783.  
 PR 29-AUG-2000; 2000US-00651236.  
 PR 06-SEP-2000; 2000US-00657279.  
 PR 02-OCT-2000; 2000US-00679426.  
 PR 10-OCT-2000; 2000US-00685166.  
 PR 09-NOV-2000; 2000US-00709729.  
 PR 12-JAN-2001; 2001US-00759143.  
 PR 09-FEB-2001; 2001US-00780669.  
 PR 09-MAY-2001; 2001US-00852911.  
 PR 29-JUN-2001; 2001US-00895814.  
 PR 10-DEC-2001; 2001US-00012896.  
 XX  
 (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
 PI Kalos MD, Fanger CR, Retter MW, Stolk JA, Day CH, Vedwick TS;  
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;  
 PI Meagher MJ, Deng T;  
 XX  
 WPI; 2003-777973/73.  
 DR P-PSDB; ADG26692.  
 XX  
 PT New polynucleotides encoding prostate specific polypeptides isolated from  
 PT a human prostate tumor cDNA library are useful to diagnose and treat  
 PT cancer particularly prostate cancer.  
 XX  
 PS Example 17; SEQ ID NO 823; 99pp; English.  
 XX  
 CC The invention relates to human prostate-specific polypeptides and the  
 CC polynucleotides encoding them. The invention also relates to an isolated  
 CC antibody or its antigen-binding fragment that specifically binds a  
 CC polypeptide of the invention, a method of detecting cancer in a patient  
 CC comprising contacting a biological sample of the patient with an agent  
 CC that binds a prostate-specific polypeptide and comparing the amount of



CC bound polypeptide compared to a predetermined cut-off value and a fusion  
CC protein comprising a prostate-specific polypeptide. The sequences of the  
CC invention are used to diagnose and treat cancer, particularly prostate  
CC cancer. This sequence represents cDNA encoding a human prostate-specific  
CC polypeptide of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification but was obtained in electronic  
CC format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX  
SQ Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
Query Match 5.4%; Score 216; DB 10; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3655 ATCCGGGAGAAATTTGCCACTGCACACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714  
DB 7 ATCCGGGAGAAATTTGCCACTGCACACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66  
QY 3715 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 3774  
DB 67 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 126  
QY 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCACAACTGGGCAG 3834  
DB 127 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCACAACTGGGCAG 186  
QY 3835 GCAGAAGCGCGTGCCTCCTCAGTGAACAGCAAAACAG 3870  
DB 187 GCAGAAGCGCGTGCCTCCTCAGTGAACAGCAAAACAG 222

RESULT 13  
ID AAX40493  
XX AAX40493 standard; cDNA; 439 BP.  
AC AAX40493;  
XX  
DT 18-JUN-1999 (first entry)  
XX  
DE Human secreted protein 5' EST SEQ ID No: 93.  
XX  
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;  
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;  
KW upstream regulatory sequence; cytokine activity; cell proliferation;  
KW differentiation; haematopoiesis regulation; tissue growth regulation;  
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;  
KW thrombolytic; anti-inflammatory; tumour inhibition; db.  
XX  
OS Homo sapiens.  
XX  
XX WO9906550-A2.  
XX  
XX 11-FEB-1999.  
XX  
XX 31-JUL-1998; 98WO-IB001232.  
XX  
XX 01-AUG-1997; 97US-00905144.  
XX  
XX (GBST ) GENSET.  
XX  
XX Dumas Milne Edwards J, Duclert A, Lacroix B;  
XX  
XX WPI: 1999-153780/13.  
XX  
XX P-PSDB; AAY11771.  
XX  
XX New isolated prostate-derived nucleic acids - used to develop products  
XX which may have cytokine, immune regulatory, haematopoiesis regulating,  
XX anti-inflammatory or tumour inhibition activity.  
XX  
XX Claim 1; Page 214-215; 675pp; English.  
XX  
XX AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for  
XX human secreted proteins expressed in prostate, and encode the proteins

CC given in AAY11716 to AAY11993 respectively. The proteins given represent  
CC the signal peptide and an N-terminal fragment of a secreted protein. The  
CC nucleic acid sequences can be used for producing secreted human gene  
CC products. They can also be used to develop products for diagnosis and  
CC therapy. The proteins obtained may have cytokine activity, cell  
CC proliferation and differentiation activity, haematopoiesis regulating  
CC activity, tissue growth regulating activity, reproductive hormone  
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and  
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, tumour inhibition activity or other activities. The products  
CC can be used in forensic, gene therapy and chromosome mapping procedures.  
CC The sequences can also be used for obtaining corresponding promoter  
CC sequences. The nucleic acids encoding the signal peptides can be used for  
CC directing extracellular secretion of a polypeptide or the insertion of a  
CC polypeptide into a membrane, or importing a polypeptide into a cell  
XX  
SQ Sequence 439 BP; 128 A; 89 C; 96 G; 122 T; 0 U; 4 Other;  
Query Match 5.3%; Score 211; DB 2; Length 439;  
Best Local Similarity 100.0%; Pred. No. 3.6e-94;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2040 GAATGTCCTCCAGTTACACTATCAGAGGAGAACCCCTCTGAAGAAAAGTGTCTTCAGGC 2099  
DB 229 GAATGTCCTCCAGTTACACTATCAGAGGAGAACCCCTCTGAAGAAAAGTGTCTTCAGGC 288  
QY 2100 CTATAAGAAATTTACTTCAGAGCTGGTCTCACTGGAATGTCTTCATTTTCTCTCTCT 2159  
DB 289 CTATAAGAAATTTACTTCAGAGCTGGTCTCACTGGAATGTCTTCATTTTCTCTCTCT 348  
QY 2160 AAACACTGCAGCTCAGGTTCCTATGCTTCAAGATTGGTGGCTTTCATATCTGGGCAA 2219  
DB 349 AAACACTGCAGCTCAGGTTCCTATGCTTCAAGATTGGTGGCTTTCATATCTGGGCAA 408  
QY 2220 CAACAAAGTATGCTAAATGCTCACTGTAAT 2250  
DB 409 CAACAAAGTATGCTAAATGCTCACTGTAAT 439  
RESULT 14  
ID ABV41670  
XX ABV41670 standard; cDNA; 391 BP.  
AC ABV41670;  
XX  
XX 16-SEP-2002 (first entry)  
DT  
XX  
XX Human prostate expression marker cDNA 41661.  
DE  
XX  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200160860-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 20-FEB-2001; 2001WO-US005171.  
XX  
XX 17-FEB-2000; 2000US-0183319P.  
XX  
XX 16-MAR-2000; 2000US-0189862P.  
XX  
XX 25-MAY-2000; 2000US-0207454P.  
XX  
XX 09-JUN-2000; 2000US-0211314P.  
XX  
XX 18-JUL-2000; 2000US-0219007P.  
XX  
XX 13-DEC-2000; 2000US-0255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI; 2001-662795/76.  
XX



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2005, 03:57:21 ; Search time 620 Seconds  
(without alignments)  
10498.563 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

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Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3973.2	99.9	4231	4	US-09-647-140B-1
2	3966	99.7	6082	3	US-09-439-313-535
3	3966	99.7	6082	4	US-09-636-215-535
4	3966	99.7	6082	4	US-09-685-166A-535
5	3966	99.7	6082	4	US-09-679-426-535
6	3966	99.7	6082	4	US-09-759-143-535
7	3966	99.7	6082	4	US-09-651-236-535
8	3977.8	95.5	6140	3	US-09-439-313-536
9	3977.8	95.5	6140	4	US-09-636-215-536
10	3977.8	95.5	6140	4	US-09-685-166A-536
11	3977.8	95.5	6140	4	US-09-679-426-536
12	3977.8	95.5	6140	4	US-09-759-143-536
13	3977.8	95.5	6140	4	US-09-651-236-536
14	1047	26.3	1074	4	US-09-636-215-824
15	1047	26.3	1074	4	US-09-685-166A-824
16	1047	26.3	1074	4	US-09-679-426-824
17	1047	26.3	1074	4	US-09-759-143-824
18	1047	26.3	1074	4	US-09-651-236-824
19	517	13.0	553	4	US-09-281-646B-27
20	517	13.0	2275	4	US-09-281-646B-1
21	435.8	11.0	4781	2	US-09-001-273-1
22	435.8	11.0	4781	3	US-08-843-459A-1
23	435.8	11.0	4847	3	US-09-061-400-1
24	435.8	11.0	5838	4	US-09-647-140B-3
25	431.2	10.8	586	4	US-09-281-646B-14
26	428.6	10.8	5696	4	US-09-976-594-335
27	390.4	9.8	5011	1	US-08-141-893-1

28	390.4	9.8	5011	1	US-08-463-092B-1	Sequence 1, Appli
29	390.4	9.8	5011	2	US-08-462-109A-1	Sequence 1, Appli
30	390.4	9.8	5011	2	US-08-460-907B-1	Sequence 1, Appli
31	390.4	9.8	5011	3	US-08-463-179A-1	Sequence 1, Appli
32	390.4	9.8	5011	3	US-08-461-384B-1	Sequence 1, Appli
33	390.4	9.8	5011	3	US-08-407-207A-1	Sequence 1, Appli
34	388.8	9.8	5011	1	US-08-463-092B-3	Sequence 3, Appli
35	388.8	9.8	5011	2	US-08-462-109A-3	Sequence 3, Appli
36	388.8	9.8	5011	2	US-08-460-907B-3	Sequence 3, Appli
37	388.8	9.8	5011	3	US-08-463-179A-3	Sequence 3, Appli
38	388.8	9.8	5011	3	US-08-461-384B-3	Sequence 3, Appli
39	377	9.5	5889	1	US-08-463-092B-5	Sequence 5, Appli
40	377	9.5	5889	2	US-08-462-109A-5	Sequence 5, Appli
41	377	9.5	5889	2	US-08-460-907B-5	Sequence 5, Appli
42	377	9.5	5889	3	US-08-463-179A-5	Sequence 5, Appli
43	377	9.5	5889	3	US-08-461-384B-5	Sequence 5, Appli
44	367	9.2	5232	3	US-08-972-927-1	Sequence 1, Appli
45	356.2	9.0	5175	3	US-08-972-927-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-647-140B-1  
; Sequence 1, Application US/09647140B  
; Patent No. 6803184  
; GENERAL INFORMATION:  
; APPLICANT: Fox Chase Cancer Center  
; APPLICANT: Kruh, Gary D.  
; APPLICANT: Lee, Kun  
; APPLICANT: Belinsky, Martin G.  
; APPLICANT: Bain, Lisa J.  
; TITLE OF INVENTION: WEP-Related ABC Transporter Encoding  
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof  
; FILE REFERENCE: FCCC 98-02  
; CURRENT APPLICATION NUMBER: US/09/647,140B  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: PCT/US99/06644  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,759  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/095,153  
; PRIOR FILING DATE: 1998-08-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4231  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-647-140B-1

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Db	176	CGCGTGTCTTCTCGTGGCTCAATCCCTTGTAAAAATTGGCCATAAACGGAGATTAG	235				
Qy	121	GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	180				
Db	236	GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	295				
Qy	181	CAAGGGTTCGGGATAAAGAGTTTAAAGAGTCTGAGATGACGACAGAGCTTCTTTA	240				
Db	296	CAAGGGTTCGGGATAAAGAGTTTAAAGAGTCTGAGATGACGACAGAGCTTCTTTA	355				
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RESULT 2
US-09-439-313-535
; Sequence 535, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Panger, Gary.
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-535

Query Match 99.7%; Score 3966; DB 3; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      2341  |||||GCAAGATCTCTATTGGTATTCTAGTCTCTGTTAACTCTTCAAACTTTTGCACAAACAAA 2400
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Qy      2401  |||||ATGTTTGAGTCAATCTCTGAAAGCTCCGGTATTATTCTTTGATGAAATCCAAATAGGAAGA 2460
Db      2586  |||||ATGTTTGAGTCAATCTCTGAAAGCTCCGGTATTATTCTTTGATGAAATCCAAATAGGAAGA 2645
Qy      2461  |||||ATTTTAAATCGTTTCTCAAAAGACATTTGGACACATTTGGATGATTTGCTGCGCTGACGTTT 2520
Db      2646  |||||ATTTTAAATCGTTTCTCAAAAGACATTTGGACACATTTGGATGATTTGCTGCGCTGACGTTT 2705
Qy      2521  |||||TTAGATTTTCATCCAGACATTTGCTACAAAGTGTGCTGTGGTCTCTGTGGCTGTGGCCGTG 2580
Db      2706  |||||TTAGATTTTCATCCAGACATTTGCTACAAAGTGTGCTGTGGTCTCTGTGGCTGTGGCCGTG 2765
Qy      2581  |||||ATTCCTTTGGATCGCAATACCCCTTGGTTCCCTTGGAAATCAATTTTCAATTTTCTCGGCGA 2640
Db      2766  |||||ATTCCTTTGGATCGCAATACCCCTTGGTTCCCTTGGAAATCAATTTTCAATTTTCTCGGCGA 2825
Qy      2641  |||||TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGGAATCTCAACTCGGAGTCCAGTG 2700
Db      2826  |||||TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGGAATCTCAACTCGGAGTCCAGTG 2885
Qy      2701  |||||TTTTTCCACATTTGTCATCTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760
Db      2886  |||||TTTTTCCACATTTGTCATCTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945
Qy      2761  |||||GAGAGGTGTGAGGAACCTGTTTGATGACACACAGGATTTACATTCAGAGGCTTGGTTCTTG 2820
Db      2946  |||||GAGAGGTGTGAGGAACCTGTTTGATGACACACAGGATTTACATTCAGAGGCTTGGTTCTTG 3005
Qy      2821  |||||TTTTTGACAGTCCCGCTGGTTCGGCTGCTCTGGATGCGATCTGTGCGCATGTTTGTGTC 2880
Db      3006  |||||TTTTTGACAGTCCCGCTGGTTCGGCTGCTCTGGATGCGATCTGTGCGCATGTTTGTGTC 3065
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Db      3066  |||||ATCATCGTTCGCTTTGGGTCCCTGATTTCTGCAAAACTCTGGATGCGGCGCAGTTGGT 3125
Qy      2941  |||||TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3000
Db      3126  |||||TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3185
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Db      3186  |||||GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATTGAATACACAGACCTTGAA 3245
Qy      3061  |||||AAAGAACCTTTGGGAATATCAGAACGCCACCCAGCCTGGCCCTCATGAGGAGTG 3120
Db      3246  |||||AAAGAACCTTTGGGAATATCAGAACGCCACCCAGCCTGGCCCTCATGAGGAGTG 3305
Qy      3121  |||||ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGTGTAAGTGAAGCAT 3180
Db      3306  |||||ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGTGTAAGTGAAGCAT 3365
Qy      3181  |||||CTGACAGCATCTAATTAATCACAAGAAAGTTGGCAATTTGGGAAGAACCCGAGCTGGA 3240
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Qy      3241  |||||AAAAGTTCCTCATCTCAGCCCTTTTATGATTTGTCAGAACCCGAGTAAATTTTGATT 3300
Db      3426  |||||AAAAGTTCCTCATCTCAGCCCTTTTATGATTTGTCAGAACCCGAGTAAATTTTGATT 3485
Qy      3301  |||||GATAAGATCTTGACAACTGAAATTTGACTTCCAGATTTAAGGAAGAAATGTCAATCATA 3360
Db      3486  |||||GATAAGATCTTGACAACTGAAATTTGACTTCCAGATTTAAGGAAGAAATGTCAATCATA 3545
Qy      3361  |||||CCTCAGGAACCTGTTTGTTCCTCGGAACAATGAGGAAACCTGGATCCCTTTAATGAG 3420
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Db      3546  |||||CCTCAGGAACCTGTTTGTTCCTCAGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605
Qy      3421  |||||CACACGATGAGGAACCTGTTGGAATGCTTACAAAGGTTACAACTTTAAAGAAACCATTCGA 3480
Db      3606  |||||CACACGATGAGGAACCTGTTGGAATGCTTACAAAGGTTACAACTTTAAAGAAACCATTCGA 3665
Qy      3481  |||||GATCTTCTCGTAAAAATGGATACCTGAATTAGCAGAATCAGGATCCAAATTTTAGTGTGGA 3540
Db      3666  |||||GATCTTCTCGTAAAAATGGATACCTGAATTAGCAGAATCAGGATCCAAATTTTAGTGTGGA 3725
Qy      3541  |||||CAAAAGAACCTGTTGCTGCTTGCAGGGCAATTTCTCAGAAAAAATCAGATATTGATTTATT 3600
Db      3726  |||||CAAAAGAACCTGTTGCTGCTTGCAGGGCAATTTCTCAGAAAAAATCAGATATTGATTTATT 3785
Qy      3601  |||||GATGAACGCGACGGCAAAATGTTGGATCCAAAGAACTCATGAGTTTAAATAC-AAAAAATCCGG 3660
Db      3786  |||||GATGAACGCGACGGCAAAATGTTGGATCCAAAGAACTCATGAGTTTAAATAC-AAAAAATCCGG 3844
Qy      3661  |||||GAGAAATTTGCCCACTGCACCGTCTAACCAATTTGCACACAGATTTGAACACCATTTATTGAC 3720
Db      3845  |||||GAGAAATTTGCCCACTGCACCGTCTAACCAATTTGCACACAGATTTGAACACCATTTATTGAC 3904
Qy      3721  |||||AGCACAAGATTAATGTTTGTAGATTCAGGAAGACTGAAAGATATGATGAGCCGTATGTT 3780
Db      3905  |||||AGCACAAGATTAATGTTTGTAGATTCAGGAAGACTGAAAGATATGATGAGCCGTATGTT 3964
Qy      3781  |||||TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGTTGCAACAACCTGGGCAAGCAGAA 3840
Db      3965  |||||TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGTTGCAACAACCTGGGCAAGCAGAA 4024
Qy      3841  |||||GCCGCTGCCCTCACTGAAAACAGCAAAAACAGGTATATCTTCAAAAAGAAATTTATCCACATTT 3900
Db      4025  |||||GCCGCTGCCCTCACTGAAAACAGCAAAAACAGGTATATCTTCAAAAAGAAATTTATCCACATTT 4084
Qy      3901  |||||GGTCACACTGACCAACATGGTTTACAAACATTCCTCAATGCAAGCCCTCGACCTTAACTATT 3960
Db      4085  |||||GGTCACACTGACCAACATGGTTTACAAACATTCCTCAATGCAAGCCCTCGACCTTAACTATT 4144
Qy      3961  |||||TTGAGACAGACACTGTGA 3978
Db      4145  |||||TTGAGACAGACACTGTGA 4162
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## RESULT 3

```
US-09-636-215-535
; Sequence 535, Application US/09636215
; Patent No. 8620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
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:   LENGTH: 6082
:   TYPE: DNA
:   ORGANISM: Homo sapiens
US-09-636-215-535

Query Match      99.7%;   Score 3966;   DB 4;   Length 6082;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 3977;   Conservative 0;   Mismatches 0;   Indels 1;   Gaps 1;

Qy   1   ATGCTGCCCGTGTACAGAGAGTGAAGCCCAACCCGCTGCAGGACGCGAAACCTCTGCTCA 60
Db   |   |||||
186   ATGCTGCCCGTGTACAGAGAGTGAAGCCCAACCCGCTGCAGGACGCGAAACCTCTGCTCA 245
Qy   |   |||||
61   CGCGTGTCTCTCGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAG 120
Db   |   |||||
246   CGCGTGTCTCTCGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAG 305
Qy   |   |||||
121   GAAGATGATATGATATTCAGTGTCTCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG 180
Db   |   |||||
306   GAAGATGATATGATATTCAGTGTCTCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG 365
Qy   |   |||||
181   CAAGGGTTCGGGATAAAGAGTTTAAAGAGCTCAGAAATGACGACAGAAAGCCCTTCTTTA 240
Db   |   |||||
366   CAAGGGTTCGGGATAAAGAGTTTAAAGAGCTCAGAAATGACGACAGAAAGCCCTTCTTTA 425
Qy   |   |||||
241   ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300
Db   |   |||||
426   ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 485
Qy   |   |||||
301   ATTGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTATTTT 360
Db   |   |||||
486   ATTGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTATTTT 545
Qy   |   |||||
361   GAAATATTATGATCCATGGATTCTGTGGCTTTGAACACAGCGGTACGCTATGCCACCGGTG 420
Db   |   |||||
546   GAAATATTATGATCCATGGATTCTGTGGCTTTGAACACAGCGGTACGCTATGCCACCGGTG 605
Qy   |   |||||
421   CTGACTTTTTCAGCTCATTTTGGCTATACCTGATCACTTATATTTTATCAGGTTTCAG 480
Db   |   |||||
606   CTGACTTTTTCAGCTCATTTTGGCTATACCTGATCACTTATATTTTATCAGGTTTCAG 665
Qy   |   |||||
481   TGTCTGGGATGAGTTACAGTAGCCATGTGCCATATGATTTATCGGAAGGCATTCGT 540
Db   |   |||||
666   TGTCTGGGATGAGTTACAGTAGCCATGTGCCATATGATTTATCGGAAGGCATTCGT 725
Qy   |   |||||
541   CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTCTCAAT 600
Db   |   |||||
726   CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTCTCAAT 785
Qy   |   |||||
601   GATGTGAACAGTTTGTATCAGTGCATGAGTGTCTTACACTTCTGTCGGCAGGACCACTG 660
Db   |   |||||
786   GATGTGAACAGTTTGTATCAGTGCATGAGTGTCTTACACTTCTGTCGGCAGGACCACTG 845
Qy   |   |||||
661   CAGCGGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTCTGGG 720
Db   |   |||||
846   CAGCGGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTCTGGG 905
Qy   |   |||||
721   ATGGAGTCTTAATCATTTCTCTGCCCTTGCAGAGCTTTTGGAAAGTTTGTCTCTCATCA 780
Db   |   |||||
906   ATGGAGTCTTAATCATTTCTCTGCCCTTGCAGAGCTTTTGGAAAGTTTGTCTCTCATCA 965
Qy   |   |||||
781   CTGAGGAGTAAATCTGCAACTTTTCCAGATGCCAGGATCAGGACCCATGAATGAAGTTATA 840
Db   |   |||||
966   CTGAGGAGTAAATCTGCAACTTTTCCAGATGCCAGGATCAGGACCCATGAATGAAGTTATA 1025
Qy   |   |||||
841   ACTGGTATAAGGATAAATAAATGTACGCCCTGGGAAAGTCAATTTCAAATCTTATTACC 900
Db   |   |||||
1026   ACTGGTATAAGGATAAATAAATGTACGCCCTGGGAAAGTCAATTTCAAATCTTATTACC 1085
Qy   |   |||||
901   AATTGTGAAGAAAGAGGATTTCCAAAGATTCGAGAGTTCTCTGCTCAGGGGATGAAT 960
Db   |   |||||
1086   AATTGTGAAGAAAGAGGATTTCCAAAGATTCGAGAGTTCTCTGCTCAGGGGATGAAT 1145

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Qy   961   TTGGCTTCGTTTTTTTCAGTGCAGCAAAATCATCTGTGTTTGTGACCTTTCACCACCTACGTG 1020
Db   |   |||||
1146   TTGGCTTCGTTTTTTTCAGTGCAGCAAAATCATCTGTGTTTGTGACCTTTCACCACCTACGTG 1205
Qy   |   |||||
1021   CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATATGGGGCT 1080
Db   |   |||||
1206   CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATATGGGGCT 1265
Qy   |   |||||
1081   GTGGGGCTGACGGTTACCTTCTTCCCTCAGCCATTCAGAGGGGTGTACAGAGCAATC 1140
Db   |   |||||
1266   GTGGGGCTGACGGTTACCTTCTTCCCTCAGCCATTCAGAGGGGTGTACAGAGCAATC 1325
Qy   |   |||||
1141   GTCAGCATCCGAAGAATCCAGAGCCCTTTTCTACTCTGATGAGATATCACAGCGCAACCGT 1200
Db   |   |||||
1326   GTCAGCATCCGAAGAATCCAGAGCCCTTTTCTGCTACTGATGAGATATCACAGCGCAACCGT 1385
Qy   |   |||||
1201   CAGCTGCGCTCAGATGGTATAAAAGATGGTGATGTGCAGGATTTTACTGCTTTTGGGAT 1260
Db   |   |||||
1386   CAGCTGCGCTCAGATGGTATAAAAGATGGTGATGTGCAGGATTTTACTGCTTTTGGGAT 1445
Qy   |   |||||
1261   AAGGCATCAGAGACCCCAACTCTCAAGGGCTTTCTTCTTACTGTACAGACCTGGCGAATTG 1320
Db   |   |||||
1446   AAGGCATCAGAGACCCCAACTCTCAAGGGCTTTCTTCTTACTGTACAGACCTGGCGAATTG 1505
Qy   |   |||||
1321   TTAGCTGTGTGTCGCCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAAGTGCCTGCTCGGG 1380
Db   |   |||||
1506   TTAGCTGTGTGTCGCCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAAGTGCCTGCTCGGG 1565
Qy   |   |||||
1381   GAATTTGCCCCCAAGTCACTGGGCTGGTGCAGCGTGCATGGAAGAAATTCCTATGTCTCTCAG 1440
Db   |   |||||
1566   GAATTTGCCCCCAAGTCACTGGGCTGGTGCAGCGTGCATGGAAGAAATTCCTATGTCTCTCAG 1625
Qy   |   |||||
1441   CAGCCCTGGGTGTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAGAAATACGAA 1500
Db   |   |||||
1626   CAGCCCTGGGTGTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAGAAATACGAA 1685
Qy   |   |||||
1501   AAGGAACGATATGAAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTTACAGCTGTG 1560
Db   |   |||||
1686   AAGGAACGATATGAAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTTACAGCTGTG 1745
Qy   |   |||||
1561   GAGGATGGTGTATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA 1620
Db   |   |||||
1746   GAGGATGGTGTATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA 1805
Qy   |   |||||
1621   GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACAGT 1680
Db   |   |||||
1806   GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACAGT 1865
Qy   |   |||||
1681   CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740
Db   |   |||||
1866   CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925
Qy   |   |||||
1741   ATTTTGCATGAGAAAGATCAAAATTTTATGTGACTCATCAGTTTGCAGTACCTCAAAAGCTGCA 1800
Db   |   |||||
1926   ATTTTGCATGAGAAAGATCAAAATTTTATGTGACTCATCAGTTTGCAGTACCTCAAAAGCTGCA 1985
Qy   |   |||||
1801   AGTCAGAGTTCTGATATTTGAAAGATGTAATGTCGAGAGGGGACTTACACTGAGTTTC 1860
Db   |   |||||
1986   AGTCAGAGTTCTGATATTTGAAAGATGTAATGTCGAGAGGGGACTTACACTGAGTTTC 2045
Qy   |   |||||
1861   CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGATAATAGAGAAAGTCAACAA 1920
Db   |   |||||
2046   CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGTATAGAGAAAGTCAACAA 2105
Qy   |   |||||
1921   CCTCCAGTTCCAGGAATCCCAACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980
Db   |   |||||
2106   CCTCCAGTTCCAGGAATCCCAACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165
Qy   |   |||||
1981   TCTCAAACAATCTTCTAGACCCCTCTGAAAGATGCTCTCTGGAGAGCCAAAGATACAGAG 2040
Db   |   |||||
2166   TCTCAAACAATCTTCTAGACCCCTCTGAAAGATGCTCTCTGGAGAGCCAAAGATACAGAG 2225
Qy   |   |||||
2041   AATGTCCCGATTACACTATACAGAGGAAACCGCTTCTGAAGGAAAGTTGGTTTTCAGGCC 2100

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Db 2226 AATGTCAGGTTACACTATACAGAGAGAACCGTCTGAAGGAAAAGTTGGTTTTTCAGGCC 2285  
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Db 2286 TATAAGAAATTAATTCAGAGCTGGTCTCACTCGATGTTGCTTCATTTTCTTATTTCTCCTA 2345  
Qy 2161 AACACTGAGCTCAGGTTGCCCTATGCTTCAAGATTTGGTGGCTTTTCACTATGCGCAAC 2220  
Db 2346 AACACTGAGCTCAGGTTGCCCTATGCTTCAAGATTTGGTGGCTTTTCACTATGCGCAAC 2405  
Qy 2221 AAAAAGATGCTAAATGCTCTGTAATGAGAGAGAAATGTAACCGAGAGCTAGAT 2280  
Db 2406 AAAAAGATGCTAAATGCTCACTGTAATGAGAGAGAAATGTAACCGAGAGCTAGAT 2465  
Qy 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2340  
Db 2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2525  
Qy 2341 GCAAGATCTTAATGGTATTTCTAGCTCTTGTAACTCTTCAAACTTTGCAACAA 2400  
Db 2526 GCAAGATCTTAATGGTATTTCTAGCTCTTGTAACTCTTCAAACTTTGCAACAA 2585  
Qy 2401 ATGTTTGAAGTCAATTTCTGAAGCTCCGGTATTAATTTCTTGTAGTAAGAAATCCAATAGGAAGA 2460  
Db 2586 ATGTTTGAAGTCAATTTCTGAAGCTCCGGTATTAATTTCTTGTAGTAAGAAATCCAATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCAAGACATTTGACACTTGGATGATTTGCTGCGCTGACGTTT 2520  
Db 2646 ATTTTAAATCGTTTCTCAAGACATTTGACACTTGGATGATTTGCTGCGCTGACGTTT 2705  
Qy 2521 TTAGATTTTCACTCAGACATTTGCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2580  
Db 2706 TTAGATTTTCACTCAGACATTTGCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2765  
Qy 2581 ATTCTTGGATGCAATACCTTTGGTCCCTTGGATTCATTTTCAATTTTCTTGGCGA 2640  
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Db 3066 ATCATCGTTGCTTGGGTCCTGATCTGCAAAAACCTCTGGATCGCGGCAGGTTGGT 3125  
Qy 2941 TTGGCACTGTCCTATGCCCTCACGCTCATNGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
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Qy 3001 GCTGAAGTTGAATATGATGATCTCAGTAGAAGGGTCAATTTGAATACACAGACTTGAA 3060  
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Qy 3061 AAAGAGCACCCTCGGAATATCAGAAACGCCACACAGCCTGSCCCCATGAAGGAGTG 3120  
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Qy 3121 ATAATCTTTGCAATGTGAATCTTCATGTACAGTCCAGGTGGGCTCTGTGTAATGAAGCAT 3180

Db 3306 ATAATCTTTGCAATGTGAACCTTTCATGTACAGTCAGGTGGGCTCTGTGTAAGCAT 3365  
Qy 3181 CTGACAGCACTCATTTAAATCAAGAAAAGGTTGCACTTGTGGGAAAGAACCGGAGCTGGA 3240  
Db 3366 CTGACAGCACTCATTTAAATCAAGAAAAGGTTGCACTTGTGGGAAAGAACCGGAGCTGGA 3425  
Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTTGTGAGAACCCGAAAGGTAATAATTTGGATT 3300  
Db 3426 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTTGTGAGAACCCGAAAGGTAATAATTTGGATT 3485  
Qy 3301 GATTAAGATCTTTGACAACTGAATTTGGACTTCCAGATTTTAAAGAGAAAATGTCAATCAT 3360  
Db 3486 GATTAAGATCTTTGACAACTGAATTTGGACTTCCAGATTTTAAAGAGAAAATGTCAATCAT 3545  
Qy 3361 CCTCAGGAACCTGTTTGTTCACCTGGAACAATAGAGAAAACCTGATCCCTTTTAAATGAG 3420  
Db 3546 CCTCAGGAACCTGTTTGTTCACCTGGAACAATAGAGAAAACCTGATCCCTTTTAAATGAG 3605  
Qy 3421 CACACGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTTAAAGAAAACCAATTGAA 3480  
Db 3606 CACACGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTTAAAGAAAACCAATTGAA 3665  
Qy 3481 GATCTTCTGTAAATTTGGATACCTGAATTTAGCAGAACTCAGGATCCCAATTTTGTGTTGGA 3540  
Db 3666 GATCTTCTGTAAATTTGGATACCTGAATTTAGCAGAACTCAGGATCCCAATTTTGTGTTGGA 3725  
Qy 3541 CAAAGACAACTGTGTGCTTCCAGGCAATCTCAGGAAAATTCAGATTTGATTTATT 3600  
Db 3726 CAAAGACAACTGTGTGCTTCCAGGCAATCTCAGGAAAATTCAGATTTGATTTATT 3785  
Qy 3601 GATGAAGCGACGGCAATTTGGAATCCTGAAGAACTGATGATGTTTAAATACAAAATAATCCGG 3660  
Db 3786 GATGAAGCGACGGCAATTTGGAATCCTGAAGAACTGATGATGTTTAAATACAAAATAATCCGG 3844  
Qy 3661 GAGAAATTTGCCCCACTGCAACCGTGTAAACATTTGCAACAGATTTGAAACCACTTTTGTGAC 3720  
Db 3845 GAGAAATTTGCCCCACTGCAACCGTGTAAACATTTGCAACAGATTTGAAACCACTTTTGTGAC 3904  
Qy 3721 AGCCACAAGATAATGTTTATAGATTTAGGAGAGCTTCAAGAGATGTAAGAGATGATGAGCCGTATGTT 3780  
Db 3905 AGCCACAAGATAATGTTTATAGATTTAGGAGAGCTTCAAGAGATGTAAGAGATGATGAGCCGTATGTT 3964  
Qy 3781 TTGCTGCAAAATAAAGAGAGCTTATTTTACAAGATGTTGCAACAACTGGGCAAGGCAAGAA 3840  
Db 3965 TTGCTGCAAAATAAAGAGAGCTTATTTTACAAGATGTTGCAACAACTGGGCAAGGCAAGAA 4024  
Qy 3841 GCCGCTGCCCTCACTGAAAACAGCAAAACAGGTATATCTTCAAAAAGAAAATTTTCCACATATT 3900  
Db 4025 GCCGCTGCCCTCACTGAAAACAGCAAAACAGGTATATCTTCAAAAAGAAAATTTTCCACATATT 4084  
Qy 3901 GGTCACTGACCACTGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 3960  
Db 4085 GGTCACTGACCACTGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 4144  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 4145 TTCGAGACAGCACTGTGA 4162

## RESULT 4

US-09-685-166A-535  
; Sequence 535, Application US/09685166A  
; Patent No. 5630305  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.

```

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-535

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Query Match 99.7%; Score 3966; DB 4; Length 6082;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 397; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 5

US-09-679-426-535

; Sequence 535, Application US/09679426

; Patent No. 6759515

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

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; APPLICANT: Kalos, Michael D.

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; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Barrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; CURRENT APPLICATION NUMBER: US/09/679,426

; CURRENT FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 895

; SOFTWARE: Fast-Seq for Windows Version 3.0

; SEQ ID NO 535

; LENGTH: 6082

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-679-426-535

Query Match 99.7%; Score 3966; DB 4; Length 6082;

Best Local Similarity 100.0%; Mismatch 0;

Matches 3977; Conservative 0; Indels 1; Gaps 1;

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Db 2046 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAAGTGAA 2105  
QY 1921 CCTCCAGTTCAGGAACCTCCACACTAAGGAATGCTACTCTCAGAGTCTTCGGTTTGG 1980  
Db 2106 CCTCCAGTTCAGGAACCTCCACACTAAGGAATGCTACTCTCAGAGTCTTCGGTTTGG 2165  
QY 1981 TCTCAACAATCTTCTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2040  
Db 2166 TCTCAACAATCTTCTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2225  
QY 2041 AATGTCCCAGTTACACTATCAGAGGAGAACCGTCTCTGAAGAAAGTTGGTTTTCAGGCC 2100  
Db 2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTCTCTGAAGAAAGTTGGTTTTCAGGCC 2285  
QY 2101 TATAAGAAATTAATTCAGAGCTGGTGCTCATCTGGATGTCCTCAATTTCTTATTCCTTA 2160  
Db 2286 TATAAGAAATTAATTCAGAGCTGGTGCTCATCTGGATGTCCTCAATTTCTTATTCCTTA 2345  
QY 2161 AACACTGCAGCTCAGGTTGGCTATGCTCTCAAGATTTGGTGGCTTTTCACTATCGGCAAC 2220  
Db 2346 AACACTGCAGCTCAGGTTGGCTATGCTCTCAAGATTTGGTGGCTTTTCACTATCGGCAAC 2405  
QY 2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAAACCGAGAAGCTAGAT 2280  
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QY 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA 2340  
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QY 2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTAACTCTTCAAACTTTTGCACAA 2400  
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QY 2401 ATGTTTGAAGTCAATCTCAAGCTCCGGTATTTATTTCTTGTAGAGAAATCCAAATAGGAAGA 2460  
Db 2586 ATGTTTGAAGTCAATCTCAAGCTCCGGTATTTATTTCTTGTAGAGAAATCCAAATAGGAAGA 2645  
QY 2461 ATTTTAAATCGTTTCTCAAAAGACATTTGACACTTTGGATGATTTGCTCCGCTGACGTTT 2520  
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QY 2521 TTAGATTTTCACAGACATTTGCTACAGTGGTGGTGGTGGTCTCTGCGCTGTGCGCGTG 2580  
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QY 2581 ATTCCTTGGATCGCAATACCTTGGTCCCTTGGAAATCAATTTTCAATTTTCTTGGCGGA 2640  
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QY 2641 TATTTTGGAAACGCTCAAGAGATGTGGAAGCGCTGGAAATCTACAACCTCGGAGTCCAGTG 2700  
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Db 2826 TATTTTGGAAACGCTCAAGAGATGTGAAAGCGCCTGGAAATCTTACAACCTCGGAGTCCAGTG 2885  
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Db 2886 TTTTCCCACTTGTCTATCTTCTCTCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945  
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QY 2821 TTTTGGACAAACGCTCCCGTGGTTCGCGTCCGTCGTCGATGTCATCTGTGCCATGTTTGTGTC 2880  
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Db 3126 TTGGCACTGTCTTATGCGCTCACGCTCATGCGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3185  
QY 3001 GCTCAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3060  
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QY 3061 AAAGAAGCACCCTTCGGAATATCAGAAACGCCACACACAGCCTGSCCCCATGAAGAGTG 3120  
Db 3246 AAAGAAGCACCCTTCGGAATATCAGAAACGCCACACACAGCCTGSCCCCATGAAGAGTG 3305  
QY 3121 ATAATCTTTTGA CAATGTGAACTTTCATGTACAGTCCAGGTGGGCTCTCGTACTGAAGCAT 3180  
Db 3306 ATAATCTTTGACAATGTGAACTTTCATGTACAGTCCAGGTGGGCTCTCGTACTGAAGCAT 3365  
QY 3181 CTGACAGCACTCATTAATCAACAGAAAGGTTGSCATTTGGGAGAAACCGGAGCTGGA 3240  
Db 3366 CTGACAGCACTCATTAATCAACAGAAAGGTTGSCATTTGGGAGAAACCGGAGCTGGA 3425  
QY 3241 AAAAGTTCCCTCATCTCAGCCCTTTTAGATTTGTGAGAACCGAGGTAAAATTTGGATT 3300  
Db 3426 AAAAGTTCCCTCATCTCAGCCCTTTTAGATTTGTGAGAACCGAGGTAAAATTTGGATT 3485  
QY 3301 GATAAGATCTTTGACAACACTGAAATTTGGACTTCCAGATTTAAGGAAGAAATGTCAATCAT 3360  
Db 3486 GATAAGATCTTTGACAACACTGAAATTTGGACTTCCAGATTTAAGGAAGAAATGTCAATCAT 3545  
QY 3361 CCTCAGGAACCTGTGTTGTTGTCATCTGGAAACATAGAGGAAAAACCTGGATCCCTTTAATGAG 3420  
Db 3546 CCTCAGGAACCTGTGTTGTTGTCATCTGGAAACATAGAGGAAAAACCTGGATCCCTTTAATGAG 3605  
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Db 3606 CACACGGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTTAAAGAAACCAATTGAA 3665  
QY 3481 GATCTTCTCGTAAAAATGGATACCTGAAATTCAGAAATCAGGATCCAATTTTAGTGTGGA 3540  
Db 3666 GATCTTCTCGTAAAAATGGATACCTGAAATTCAGAAATCAGGATCCAATTTTAGTGTGGA 3725  
QY 3541 CAAAGA CAACCTGTGCTGCTTTCAGGGCAATTCCTCAGGAAAAATCAGATATGATTTATTT 3600  
Db 3726 CAAAGA CAACCTGTGCTGCTTTCAGGGCAATTCCTCAGGAAAAATCAGATATGATTTATTT 3785  
QY 3601 GATCAAGCGGCGCAATGTCGATCCCAAGACTGATGATTTAATACAAAAAAAATCCGG 3660  
Db 3786 GATCAAGCGGCGCAATGTCGATCCCAAGACTGATGATTTAATAC - AAAAAAAAATCCGG 3844  
QY 3661 GAGAAAAATTTGCGCACTGCAACCGTGTCAACCAATTCGACACAGATTTGAAACCACTATTGAC 3720  
Db 3845 GAGAAAAATTTGCGCACTGCAACCGTGTCAACCAATTCGACACAGATTTGAAACCACTATTGAC 3904  
QY 3721 AGCGACAAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGACCGGTATGTT 3780  
Db 3905 AGCGACAAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGACCGGTATGTT 3964

Qy 3781 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3840  
 Db 3965 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024  
 Qy 3841 GCCGCTGCCCTCACTGAACACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT 3900  
 Db 4025 GCCGCTGCCCTCACTGAACACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT 4084  
 Qy 3901 GGTCACTGACACATGGTTTACAAACACATTCCTCAATGGACAGCCCTCGACCTTAACTATT 3960  
 Db 4085 GGTCACTGACACATGGTTTACAAACACATTCCTCAATGGACAGCCCTCGACCTTAACTATT 4144  
 Qy 3961 TTCGAGACAGCAGTGTA 3978  
 Db 4145 TTCGAGACAGCAGTGTA 4162

RESULT 6  
 US-09-759-143-535  
 ; Sequence 535, Application US/09759143  
 ; Patent No. 6800746  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Devin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqui  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.427C23  
 ; CURRENT APPLICATION NUMBER: US/09/759.143  
 ; CURRENT FILING DATE: 2001-01-12  
 ; NUMBER OF SEQ ID NOS: 934  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 535  
 ; LENGTH: 6082  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-759-143-535

Query Match 99.7%; Score 3966; DB 4; Length 6082;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGCTGCCGCTGACAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGTCTCA 60  
 Db 186 ATGCTGCCGCTGACAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGTCTCA 245  
 Qy 61 CGCGTGTCTCTGGTGGCTCAATCCCTTGTTTAAATTTGCCATAACGGAGATTAGAG 120  
 Db 246 CGCGTGTCTCTGGTGGCTCAATCCCTTGTTTAAATTTGCCATAACGGAGATTAGAG 305  
 Qy 121 GAAGATGATATGATTCAGTCTGCGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 180  
 Db 306 GAAGATGATATGATTCAGTCTGCGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 365  
 Qy 181 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTTA 240  
 Db 366 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTTA 425

Qy 241 ACAAGACCAATCATAAAGTGTACTAGGAAATCTTAATTTAGTTTGGGAATTTTACGTTA 300  
 Db 426 ACAAGACCAATCATAAAGTGTACTAGGAAATCTTAATTTAGTTTGGGAATTTTACGTTA 485  
 Qy 301 ATTGAGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAAATTAATTAATTTT 360  
 Db 486 ATTGAGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAAATTAATTAATTTT 545  
 Qy 361 GAAATTTATGATCCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCCTATGCCACGGTG 420  
 Db 546 GAAATTTATGATCCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCCTATGCCACGGTG 605  
 Qy 421 CTGACTTTTTCAGCGCTCAATTTTGGCTATATCTGACATCACTATATTTTATCAAGTTTCA 480  
 Db 606 CTGACTTTTTCAGCGCTCAATTTTGGCTATATCTGACATCACTATATTTTATCAAGTTTCA 665  
 Qy 481 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACCTTCGT 540  
 Db 666 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACCTTCGT 725  
 Qy 541 CTTAGTAAACATGCGCATGGGAAAGACCAACACAGGCCAGATAGTCAATCTGCTGTCCAAT 600  
 Db 726 CTTAGTAAACATGCGCATGGGAAAGACCAACACAGGCCAGATAGTCAATCTGCTGTCCAAT 785  
 Qy 601 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACCACTG 660  
 Db 786 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACCACTG 845  
 Qy 661 CAGCGCATCGAGTACTGCCCTACTCTGATGGAGATAGGAATATCGTGCCTTGTCTGGG 720  
 Db 846 CAGCGCATCGAGTACTGCCCTACTCTGATGGAGATAGGAATATCGTGCCTTGTCTGGG 905  
 Qy 721 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAAGCTGTTTGGGAAGTTGTTCTCATCA 780  
 Db 906 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAAGCTGTTTGGGAAGTTGTTCTCATCA 965  
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 Qy 841 ACTGGTATAAGGATAATAAAATGTAGCGCTGGGAAAGTCATTTTCAATCTTTATTAACC 900  
 Db 1026 ACTGGTATAAGGATAATAAAATGTAGCGCTGGGAAAGTCATTTTCAATCTTTATTAACC 1085  
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 Db 1086 AATTTGAGAAAGAGGAGATTTCAGAGTTCTGAGAGTTCTCGCTCAGGAGGATCAAT 1145  
 Qy 961 TTGGCTTTCGTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTTCACCACCTAGCTG 1020  
 Db 1146 TTGGCTTTCGTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTTCACCACCTAGCTG 1205  
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 Db 1206 CTCTCGGCAAGTGTGATCACAGCCAGCCGCTGTTTCTGGCAGTGACGCTGTATGGGGCT 1265  
 Qy 1081 GTGGGGCTGAGCGTTACCTCTTCTCCCTCAGCCATTCAGAGGGTGTGAGAGGCAATC 1140  
 Db 1266 GTGGGGCTGAGCGTTACCTCTTCTCCCTCAGCCATTCAGAGGGTGTGAGAGGCAATC 1325  
 Qy 1141 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTTCATGATGATATCACAGCGCAACCGT 1200  
 Db 1326 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTTCATGATGATATCACAGCGCAACCGT 1385  
 Qy 1201 CAGCTGCCGTGAGATGGTAAAGAGATGGTGCAATGTGAGGATTTTATCTGCTTTTGGGAT 1260  
 Db 1386 CAGCTGCCGTGAGATGGTAAAGAGATGGTGCAATGTGAGGATTTTATCTGCTTTTGGGAT 1445  
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 Db 1446 AAGGCATCAGAGACCCCACTTACAGGCGCTTTCCTTACTGTACAGCCTGGGCAATTG 1505  
 Qy 1321 TTAGCTGTGGTTCGGCCCCCGTGGGAGCAGGGAAGTCACTGTTTAAAGTGGCTGCTCGG 1380



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Db 1566 GAATTTGGCCCCAAGTCACGGGCTGGTCAGCGTGCAATGGGAATTCCTATGTGCTCTCAG 1625  
Qy 1441 CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAA 1500  
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Qy 1501 AAGGAACGATATGAAGGCTGTAAGGCTGTGCTCTGAAAAGGATTTACAGCTGTTG 1560  
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Qy 1561 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA 1620  
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Qy 1681 CCTCTCAGTCAGTAGATCGGGAAGTTAGCAGACACTTGTGGAACCTGTGTATTTGTCAA 1740  
Db 1866 CCTCTCAGTCAGTAGATCGGGAAGTTAGCAGACACTTGTGGAACCTGTGTATTTGTCAA 1925  
Qy 1741 ATTTTGCATGAGAAGATCACAAATTTTGTAGTCACTCACTGTTGAGTACCTCAAGAGCTGCA 1800  
Db 1926 ATTTTGCATGAGAAGATCACAAATTTTGTAGTCACTCACTGTTGAGTACCTCAAGAGCTGCA 1985  
Qy 1801 AGTCAGATTTCTGATPATTTGAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTC 1860  
Db 1986 AGTCAGATTTCTGATPATTTGAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTC 2045  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAGTGAACAA 1920  
Db 2046 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAGTGAACAA 2105  
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Db 2226 AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAGGAAGTGGTTTTCAGGCC 2285  
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Db 2286 TATAAGAAATTAATTCAGAGCTGGTGCTCACTGGATGCTCTCAATTTTCTTATTTCTCCTA 2345  
Qy 2161 AACACTGCAGTTCAGGTTGCTATGCTCTCAAGATTTGGTGGCTTTTCATACTGGGCAAC 2220  
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Qy 2221 AAACAAAGTATGCTAAATGCTCACTGTAATGGAGGAGAAATGTAACCGAAGAGCTAGAT 2280  
Db 2406 AAACAAAGTATGCTAAATGCTCACTGTAATGGAGGAGAAATGTAACCGAAGAGCTAGAT 2465  
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Db 2466 CTTAACTGCTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 2525  
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Db 2526 GCAAGATCTCTATTTGGTATTTACGCTCTGTTAACTCTTCAAAAATTTGCAACAAA 2585  
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Db |||||

Db 2586 ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTAATTTCTTTGTATGAATAATCCAATAGGAAGA 2645  
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Db 2706 TTAGATTTTCATCCAGACATTTGCTCAAGTGGTTGGTGTGTTCTCTGTGGCTGTGGCCGCTG 2765  
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Qy 3001 GCTGAAGTCTCAGGAATATGATGATCTCAGTAGAAGGGTCAATGTAATACACAGACCTTGAA 3060  
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Db 3486 GATAAGATCTTGACAACTGAAATTTGACATTCAGATTTTAAAGGAAGAAATGTCAATCATA 3545  
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Qy 3421 CACACGGATGAGGAACCTGTGGAATGCTTACAAAGAGGTACAACTTAAAGAAACCATTTGAA 3480  
Db 3606 CACACGGATGAGGAACCTGTGGAATGCTTACAAAGAGGTACAACTTAAAGAAACCATTTGAA 3665  
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 Db 3726 CAAAGACAACTGGTGTGCTTGGCCAGGCAATTCAGGAAATCAGATATTGATTA 3785  
 Qy 3601 GATGAAGCGACGGCAATGTGGATCCAGAACTGATGAGTTAAATACAAAATAATCCGG 3660  
 Db 3786 GATGAAGCGACGGCAATGTGGATCCAGAACTGATGAGTTAAATACAAAATAATCCGG 3844  
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 Db 4025 GCGCTGCCCTCACTGAAACAGCAAAAACAGGTATATCTTCAAAAGAAATATCCACATATT 4084  
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 Db 4085 GGTCACTGACCATGCTTACAAACACTTCCAACTGAGAGCGCTCGACCTTAACTATT 4144  
 Qy 3961 TTCGAGACAGCACTGTGA 3978  
 Db 4145 TTCGAGACAGCACTGTGA 4162

RESULT 7

US-09-651-236-535  
 ; Sequence 535, Application US/09651236  
 ; Patent No. 6818751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.42718C18  
 ; CURRENT APPLICATION NUMBER: US/09/651,236  
 ; CURRENT FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 865  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 535  
 ; LENGTH: 6082  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-651-236-535

Query Match 99.7%; Score 3966; DB 4; Length 6082;  
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; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439.313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 536
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4535)
; OTHER INFORMATION: n=A,T,C or G
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Query Match      95.5%; Score 3797.8; DB 3; Length 6140;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9

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US-09-636-215-536
; Sequence 536 Application US/09636215
; Patent No. 8620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

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; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-636-215-536

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Query Match 95.5% Score 3797,8; DB 4; Length 6140;
Best Local Similarity 99.9% Pred. No. 0;
Matches 3799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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; Sequence 536, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

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; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-685-166A-536

Query Match 95.5%; Score 3797.8; DB 4; Length 6140;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 11

US-09-679-426-536

; Sequence 536, Application US/09679426

; Patent No. 6759515

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
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 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.427C20  
 ; CURRENT APPLICATION NUMBER: US/09/679,426  
 ; CURRENT FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 895  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 536  
 ; LENGTH: 6140  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(6140)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; US-09-679-426-536

Query Match 95.5%; Score 3797.8; DB 4; Length 6140;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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; Sequence 536, Application US/09759143  
; Patent No. 6800746  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 536  
; LENGTH: 6140  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(6140)  
; OTHER INFORMATION: n=A, T, C or G  
US-09-759-143-536  
Query Match 95.5%; Score 3797.8; DB 4; Length 6140;  
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 ; Patent No. 8818751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
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 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.42718C18  
 ; CURRENT APPLICATION NUMBER: US/09/651.236  
 ; CURRENT FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 865  
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 ; SEQ ID NO 536  
 ; LENGTH: 6140  
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 ; OTHER INFORMATION: n=A,T,C or G  
 US-09-651-236-536  
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Qy 2774 AACTGTTTGTATGCAACACAGGATTTACATTCAGAGGCTTGGTCTCTGTTTGTGACAACTG 2833
Db 2933 AACTGTTTGTATGCAACACAGGATTTACATTCAGAGGCTTGGTCTCTGTTTGTGACAACTG 2992
Qy 2834 CCGCTGGTTCCGCGTCCGCTCGATGCCATCTGTGCGATGTTTGTTCATCATCGTTGCCCT 2893
Db 2993 CCGCTGGTTCCGCGTCCGCTCGATGCCATCTGTGCGATGTTTGTTCATCATCGTTGCCCT 3052
Qy 2894 TTGGGTCCCTGATTCCTGCAAAAATCTCTGATGCCGGGAGGTTGGTTCGCACTGTCCT 2953
Db 3053 TTGGGTCCCTGATTCCTGCAAAAATCTCTGATGCCGGGAGGTTGGTTCGCACTGTCCT 3112
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Db 3113 ATGCCCTCAGCCTCATCGGGATGTTTCAGTGGTGTGTTTCGACAAAGTCTGAAAGTTGAGA 3172
Qy 3014 ATATGATGATCTAGTAGAAGGTCAATGATACACAGACCTTGAAAGAGAGACACTT 3073
Db 3173 ATATGATGATCTAGTAGAAGGTCAATGATACACAGACCTTGAAAGAGAGACACTT 3232
Qy 3074 GGGAAATACAGAAAGCCACACAGCCTGGCCCATGAAGAGTGTATATCTTTGACA 3133
Db 3233 GGGAAATACAGAAAGCCACACAGCCTGGCCCATGAAGAGTGTATATCTTTGACA 3292
Qy 3134 ATGTGAATCTCATGTACAGTCCAGTGGGCTCTGTACTGAAGCATCTGACAGCACTCA 3193
Db 3293 ATGTGAATCTCATGTACAGTCCAGTGGGCTCTGTACTGAAGCATCTGACAGCACTCA 3352
Qy 3194 TTAATACAGAAAGGTTGGCATTTGTGGAGAACCGGAGCTGGAAAAAGTTCCCTCA 3253
Db 3353 TTAATACAGAAAGGTTGGCATTTGTGGAGAACCGGAGCTGGAAAAAGTTCCCTCA 3412
Qy 3254 TCTCAGCCCTTTTGTAGATTTGTGAGAACCCGAGGTAAATTTGGATTGATAAGATCTTGA 3313
Db 3413 TCTCAGCCCTTTTGTAGATTTGTGAGAACCCGAGGTAAATTTGGATTGATAAGATCTTGA 3472
Qy 3314 CAATGAAATTTGGACTTCAGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTG 3373
Db 3473 CAATGAAATTTGGACTTCAGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTG 3532
Qy 3374 TTTTGTCTAGTGGAAATGAGGAAATCCCTGGATCCCTTTATGAGCAGACCGATGAGG 3433
Db 3533 TTTTGTCTAGTGGAAATGAGGAAATCCCTGGATCCCTTTATGAGCAGACCGATGAGG 3592
Qy 3434 AACTGTGGATGCTTCAAGAGGTGCAACTTAAAGAAACCATTTGAAGATCTTCTCGGTA 3493
Db 3593 AACTGTGGATGCTTCAAGAGGTGCAACTTAAAGAAACCATTTGAAGATCTTCTCGGTA 3652
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Db 3653 AAATGGATACGAAATGAGCAATCAGGATCCAAATTTTGTGTTGGCAAGAGCAACTGG 3712
Qy 3554 TGTGCTTGCAGGCAATCTCAGGAAATCAGATATTGATTTATGATGAAGCAGCG 3613
Db 3713 TGTGCTTGCAGGCAATCTCAGGAAATCAGATATTGATTTATGATGAAGCAGCG 3772
Qy 3614 CAAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAAATCCCGGAGAAATTTGCC 3673

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RESULT 14

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US-09-636-215-824
; Sequence 824, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-824

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Query Match 26.3%; Score 1047; DB 4; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 TCAGCCATTGAGAGGGTGTCTAGAGGCAATCGTCAGCATCCGAAAGATCCAGACCTTTTG 63
Qy 1171 CTACTTGATGAGATATCAGACGCAACCGTCAGTGCCTGCGTCAGATGTTAAAGATGGTG 1230
Db 64 CTACTTGATGAGATATCAGACGCAACCGTCAGTGCCTGCGTCAGATGTTAAAGATGGTG 123
Qy 1231 CATGTGCAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCACTCTCAAGAGC 1290
Db 124 CATGTGCAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCACTCTCAAGAGC 183
Qy 1291 CTTTCTCTTACTGTCTAGACCTGGCGAATTTTGTAGTGTGTGCGCCCGCTGGGAGCAGGG 1350
Db 184 CTTTCTCTTACTGTCTAGACCTGGCGAATTTTGTAGTGTGTGCGCCCGCTGGGAGCAGGG 243

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1351 AAGTCATCACTGTTAAGTGCCTGCTCGGGAAATGGCCCAAGTCACGGCTGGTCAGC 1410
1411 GTGCATGGAAGAAATGCCATGTGTCTCAGCAGCCCTGGGTGTTCTCGGAACTCTGAGG 1470
304 GTGCATGGAAGAAATGCCATGTGTCTCAGCAGCCCTGGGTGTTCTCGGAACTCTGAGG 363
1471 AGTAATATTTTATTTGGGAAGAAATACGAAAGGAACGATATGAAAGATCATAAAGGCT 1530
364 AGTAATATTTTATTTGGGAAGAAATACGAAAGGAACGATATGAAAGATCATAAAGGCT 423
1531 TGCTCTCTGAAAGAAATTTACAGCTGTTGGAGGATGTTGATCTGACTGTGATAGGAGAT 1590
424 TGCTCTCTGAAAGAAATTTACAGCTGTTGGAGGATGTTGATCTGACTGTGATAGGAGAT 483
1591 CGGGGAACCACTGAGTGGAGGGGAGAAAGCAGCGGTAAACCTTGCAGAGCAGTGTAT 1650
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544 CAAGATGCTGACATCTCTCTCGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGC 603
1711 AGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAAGATCACAAATTTTAGTG 1770
604 AGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAAGATCACAAATTTTAGTG 663
1771 ACTCATCAGTTGCAAGTACCTCAAGCTGCAAGTGCAGATCTGATATTTGAAAGATGTTAAA 1830
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1831 ATGGTGCAAGGGGACTTACACTGAGTTCCTTAAATCTGATATGATTTTGGCTCCCTT 1890
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1951 AATCGTACCTTCTCAGAGTCTCGGTTTGGTCTCAACAACTTCTAGACCTCTCTGAAA 2010
844 AATCGTACCTTCTCAGAGTCTCGGTTTGGTCTCAACAACTTCTAGACCTCTCTGAAA 903
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2071 CGTTCTGAAGGAAAGTTGGTTTTCAGGCTTATAGAAATTAATCTTACAGAGTTCAG 2130
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RESULT 15

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US-09-685-166A-824
; Sequence 824, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.

```

```

; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-824

Query Match      26.3%; Score 1047; DB 4; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1111 TCAGCCATTGAGAGGGTGTCTAGAGGCAATCGTCAGCATCCGAAAGATCCAGACCTTTTGG 1170
Db 4 TCAGCCATTGAGAGGGTGTCTAGAGGCAATCGTCAGCATCCGAAAGATCCAGACCTTTTGG 63
Qy 1171 CTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCGTCAGATGTTAAAAGATGGTG 1230
Db 64 CTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCGTCAGATGTTAAAAGATGGTG 123
Qy 1231 CATGTGCAAGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCAACTCTCAAGGC 1290
Db 124 CATGTGCAAGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCAACTCTCAAGGC 183
Qy 1291 CTTTCTTTTACTGTGCAAGCTTGGCGAAATTTAGTCTGTGTCGCGCCCGTGGGACAGGG 1350
Db 184 CTTTCTTTTACTGTGCAAGCTTGGCGAAATTTAGTCTGTGTCGCGCCCGTGGGACAGGG 243
Qy 1351 AAGTCATCACTGTTAAGTGCCTGCTCGGGAAATTTGGCCCAAGTCACGGCTGGTCAGC 1410
Db 244 AAGTCATCACTGTTAAGTGCCTGCTCGGGAAATTTGGCCCAAGTCACGGCTGGTCAGC 303
Qy 1411 GTGCATGGAAGAAATTTGCTATGCTCTCAGCAGCCCTGGGTGTTCTCGGAACTCTGAGG 1470
Db 304 GTGCATGGAAGAAATTTGCTATGCTCTCAGCAGCCCTGGGTGTTCTCGGAACTCTGAGG 363
Qy 1471 AGTAATATTTTATTTGGGAAGAAATACGAAAGGAACGATATGAAAGATCATAAAGGCT 1530
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Qy 1531 TGCTCTCTGAAAGAAATTTTACAGCTGTTGGAGGATGTTGATCTGACTGTGATAGGAGAT 1590
Db 424 TGCTCTCTGAAAGAAATTTTACAGCTGTTGGAGGATGTTGATCTGACTGTGATAGGAGAT 483
Qy 1591 CGGGGAACCACTGAGTGGAGGGGAGAAAGCAGCGGTAAACCTTGCAGAGCAGTGTAT 1650
Db 484 CGGGGAACCACTGAGTGGAGGGGAGAAAGCAGCGGTAAACCTTGCAGAGCAGTGTAT 543
Qy 1651 CAAGATGCTGACATCTATCTCTCGGAGGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGC 1710
Db 544 CAAGATGCTGACATCTATCTCTCGGAGGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGC 603
Qy 1711 AGACACTTGTTCGAACTGTGTATTTTGTCAAAATTTTGCATGAGAAAGATCACAAATTTTAGTG 1770
Db 604 AGACACTTGTTCGAACTGTGTATTTTGTCAAAATTTTGCATGAGAAAGATCACAAATTTTAGTG 663
Qy 1771 ACTCATCAGTTGCAAGTACCTCAAGCTGCAAGTGCAGATCTGATATTTGAAAGATGTTAAA 1830
Db 664 ACTCATCAGTTGCAAGTACCTCAAGCTGCAAGTGCAGATCTGATATTTGAAAGATGTTAAA 723
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Qy	1951		AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCTTGAAA	2010
Db	844		AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCTTGAAA	903
Qy	2011		GATGGTGCTCTGGAGAGCCCAAGATACAGAGAATGTCCAGTTACACTATCAGAGGAGAAC	2070
Db	904		GATGGTGCTCTGGAGAGCCCAAGATACAGAGAATGTCCAGTTACACTATCAGAGGAGAAC	963
Qy	2071		CGTTCTGAAGGAAAGTTGGTTTTCAGGCCTATAAGAAATTACTTCAGAGCTGGTGCTCAC	2130
Db	964		CGTTCTGAAGGAAAGTTGGTTTTCAGGCCTATAAGAAATTACTTCAGAGCTGGTGCTCAC	1023
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OM nucleic - nucleic search, using sw model

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Perfect score: 3978

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	216	5.4	291	US-09-636-215-823	Sequence 823, App
3	216	5.4	291	US-09-685-166A-823	Sequence 823, App
4	216	5.4	291	US-09-679-426-823	Sequence 823, App
5	216	5.4	291	US-09-759-143-823	Sequence 823, App
6	216	5.4	291	US-09-651-236-823	Sequence 823, App
7	28	0.7	34	US-09-636-215-831	Sequence 831, App
8	28	0.7	34	US-09-685-166A-831	Sequence 831, App
9	28	0.7	34	US-09-679-426-831	Sequence 831, App
10	28	0.7	34	US-09-759-143-831	Sequence 831, App
11	28	0.7	34	US-09-651-236-831	Sequence 831, App
12	24	0.6	35	US-09-636-215-828	Sequence 828, App
13	24	0.6	35	US-09-685-166A-828	Sequence 828, App
14	24	0.6	35	US-09-679-426-828	Sequence 828, App
15	24	0.6	35	US-09-759-143-828	Sequence 828, App
16	24	0.6	35	US-09-651-236-828	Sequence 828, App
17	24	0.6	36	US-09-636-215-820	Sequence 820, App
18	24	0.6	36	US-09-685-166A-820	Sequence 820, App
19	24	0.6	36	US-09-679-426-820	Sequence 820, App
20	24	0.6	36	US-09-759-143-820	Sequence 820, App
21	24	0.6	36	US-09-651-236-820	Sequence 820, App
22	24	0.6	38	US-09-636-215-830	Sequence 830, App
23	24	0.6	38	US-09-685-166A-830	Sequence 830, App
24	24	0.6	38	US-09-679-426-830	Sequence 830, App
25	24	0.6	38	US-09-759-143-830	Sequence 830, App
26	24	0.6	38	US-09-651-236-830	Sequence 830, App
27	21	0.5	340	US-09-281-646B-15	Sequence 15, Appl

28	19	0.5	19	4	US-09-281-646B-5	Sequence 5, Appli
c 29	19	0.5	418	4	US-09-621-976-17084	Sequence 17084, A
c 30	19	0.5	453	4	US-09-909-595-13	Sequence 13, Appl
c 31	18	0.5	18	4	US-09-281-646B-6	Sequence 6, Appli
c 32	18	0.5	340	4	US-10-012-282-7	Sequence 7, Appli
c 33	18	0.5	340	4	US-10-012-282-8	Sequence 8, Appli
c 34	18	0.5	445	4	US-09-621-976-8389	Sequence 8389, Ap
c 35	18	0.5	472	4	US-09-621-976-18552	Sequence 18552, A
c 36	17	0.4	20	4	US-09-198-452A-2198	Sequence 2198, Ap
c 37	17	0.4	20	4	US-09-198-452A-2200	Sequence 2200, Ap
c 38	17	0.4	25	4	US-09-396-196G-93740	Sequence 93740, A
c 39	17	0.4	35	3	US-09-333-611-5	Sequence 5, Appli
c 40	17	0.4	64	4	US-09-513-999C-22958	Sequence 22958, A
c 41	17	0.4	143	4	US-09-513-999C-34244	Sequence 34244, A
c 42	17	0.4	176	4	US-09-513-999C-19865	Sequence 19865, A
c 43	17	0.4	216	4	US-09-107-433-1965	Sequence 1965, Ap
c 44	17	0.4	246	4	US-09-543-681A-3465	Sequence 3465, Ap
c 45	17	0.4	261	4	US-08-956-171E-2654	Sequence 2654, Ap

ALIGNMENTS

RESULT 1  
US-09-281-646B-28  
; Sequence 28, Application US/09281646B  
; Patent No. 6759238  
; GENERAL INFORMATION:  
; APPLICANT: Schuetz, John  
; APPLICANT: Friedland, Arnold  
; TITLE OF INVENTION: MULTIDRUG RESISTANCE ASSOCIATED PROTEINS AND USES THEREOF  
; FILE REFERENCE: SJ-0020  
; CURRENT APPLICATION NUMBER: US/09/281.646B  
; CURRENT FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 28  
; LENGTH: 443  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-281-646B-28

Query Match	6.5%	Score 260;	DB 4;	Length 443;
Best Local Similarity	100.0%;	Pred. No. 1.4e-119;		
Matches 260;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
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Qy	3779	TTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAGGCGAG	3838	
Db	61	TTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAGGCGAG	120	
Qy	3839	AAGCGCTGCGCTCACTGAAACAGGATATCTTCAAAAGAAATTTATCCACATA	3898	
Db	121	AAGCGCTGCGCTCACTGAAACAGGATATCTTCAAAAGAAATTTATCCACATA	180	
Qy	3899	TTGCTACACTGACCATGTTTACAACACTTCCATGGACAGCCCTCGACCTTAATA	3958	
Db	181	TTGCTACACTGACCATGTTTACAACACTTCCATGGACAGCCCTCGACCTTAATA	240	
Qy	3959	TTTTCGAGACGACACTGTGA	3978	
Db	241	TTTTCGAGACGACACTGTGA	260	

RESULT 2  
US-09-636-215-823  
; Sequence 823, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.42717C17  
CURRENT APPLICATION NUMBER: US/09/636,215  
CURRENT FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 852  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 823  
LENGTH: 291  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-636-215-823

Query Match 5.4%; Score 216; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 7 ATCCGGAGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66  
Qy 3715 ATTGACAGCGACAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCG 3774  
Db 67 ATTGACAGCGACAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCG 126  
Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 186  
Qy 3835 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 222

RESULT 3  
US-09-685-166A-823  
Sequence 823, Application US/09685166A  
Patent No. 6763035  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C21  
CURRENT APPLICATION NUMBER: US/09/685,166A  
CURRENT FILING DATE: 2000-10-10  
NUMBER OF SEQ ID NOS: 898  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 823  
LENGTH: 291  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-685-166A-823

Query Match 5.4%; Score 216; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3655 ATCCGGAGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGAGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66  
Qy 3715 ATTGACAGCGACAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCG 3774  
Db 67 ATTGACAGCGACAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCG 126  
Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 186  
Qy 3835 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 222

RESULT 4  
US-09-679-426-823  
Sequence 823, Application US/09679426  
Patent No. 6759515  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C20  
CURRENT APPLICATION NUMBER: US/09/679,426  
CURRENT FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 895  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 823  
LENGTH: 291  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-679-426-823

Query Match 5.4%; Score 216; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3655 ATCCGGAGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714

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Db      7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66
QY     3715 ATTGACAGCGACAAGATAATGTTTGTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 3774
Db      67 ATTGACAGCGACAAGATAATGTTTGTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 126
QY     3775 TATGTTTTGCTGCAAAATAAAGAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834
Db     127 TATGTTTTGCTGCAAAATAAAGAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186
QY     3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db     187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222

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RESULT 5

US-09-759-143-823

; Sequence 823, Application US/09759143

; Patent No. 6800746

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427223

; CURRENT APPLICATION NUMBER: US/09759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 823

; LENGTH: 291

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-759-143-823

Query Match 5.4%; Score 216; DB 4; Length 291;

Best Local Similarity 100.0%; Pred. No. 1.6e-97;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY     3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714
Db      7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66

```

```

QY     3715 ATTGACAGCGACAAGATAATGTTTGTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 3774
Db      67 ATTGACAGCGACAAGATAATGTTTGTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 126

```

```

QY     3775 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834
Db     127 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186

```

```

QY     3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db     187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222

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RESULT 6

US-09-651-236-823

; Sequence 823, Application US/09651236

; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 823

; LENGTH: 291

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-651-236-823

Query Match 5.4%; Score 216; DB 4; Length 291;

Best Local Similarity 100.0%; Pred. No. 1.6e-97;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY     3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714
Db      7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66

```

```

QY     3715 ATTGACAGCGACAAGATAATGTTTGTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 3774
Db      67 ATTGACAGCGACAAGATAATGTTTGTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCGG 126

```

```

QY     3775 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834
Db     127 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186

```

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QY     3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db     187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222

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RESULT 7

US-09-636-215-831/c

; Sequence 831, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

```
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 831
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-636-215-831
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Query Match 0.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2130 CTGGATTGCTTCATTTTCCTTATTC 2157
Db 34 CTGGATTGCTTCATTTTCCTTATTC 7
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RESULT 8
US-09-685-166A-831/c
; Sequence 831, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 831
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-685-166A-831
```

```
Query Match 0.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2130 CTGGATTGCTTCATTTTCCTTATTC 2157
Db 34 CTGGATTGCTTCATTTTCCTTATTC 7
```

```
RESULT 9
US-09-679-426-831/c
; Sequence 831, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 831
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-679-426-831
```

```
Query Match 0.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 2130 CTGGATTGCTTCATTTTCCTTATTC 2157
Db 34 CTGGATTGCTTCATTTTCCTTATTC 7
```

```
RESULT 10
US-09-759-143-831/c
; Sequence 831, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
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; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 831  
; LENGTH: 34  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-759-143-831

Query Match 0.7%; Score 28; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2130 CTGATTGCTTCATTTTCCTTATTC 2157  
Db 34 CTGATTGCTTCATTTTCCTTATTC 7

RESULT 11  
US-09-651-236-831/c  
; Sequence 831, Application US/09651236  
; Patent No. 6818751

; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42718C18  
; CURRENT APPLICATION NUMBER: US/09/651,236  
; CURRENT FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 885  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 831  
; LENGTH: 34  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-651-236-831

Query Match 0.7%; Score 28; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2130 CTGATTGCTTCATTTTCCTTATTC 2157  
Db 34 CTGATTGCTTCATTTTCCTTATTC 7

RESULT 12  
US-09-636-215-828  
; Sequence 828, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215  
; CURRENT FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 852  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 828  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-636-215-828

Query Match 0.6%; Score 24; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAAATTTGCCCACTGC 3678  
Db 12 ATCCGGAGAAATTTGCCCACTGC 35

RESULT 13  
US-09-685-166A-828  
; Sequence 828, Application US/09685166A  
; Patent No. 6630305  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C21  
; CURRENT APPLICATION NUMBER: US/09/685,166A  
; CURRENT FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 898  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 828  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

```
; OTHER INFORMATION: PCR primer
US-09-685-166A-828

Query Match      0.6%; Score 24; DB 4; Length 35;
Best Local Similarity 100.0%; Pred.No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTGCCCACTGC 3678
Db 12 ATCCGGGAGAAATTGCCCACTGC 35

RESULT 14
US-09-679-426-828
; Sequence 828, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 828
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-679-426-828

Query Match      0.6%; Score 24; DB 4; Length 35;
Best Local Similarity 100.0%; Pred.No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTGCCCACTGC 3678
Db 12 ATCCGGGAGAAATTGCCCACTGC 35

RESULT 15
US-09-759-143-828
; Sequence 828, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
```

```
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 828
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-759-143-828

Query Match      0.6%; Score 24; DB 4; Length 35;
Best Local Similarity 100.0%; Pred.No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTGCCCACTGC 3678
Db 12 ATCCGGGAGAAATTGCCCACTGC 35

Search completed: May 20, 2005, 03:57:15
Job time : 621 secs
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 23:49:26 ; Search time 16742 Seconds  
(without alignments)  
11513.251 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcgcgtgtaccagga.....ttttcgagacgactgtga 3978

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3973.2	99.9	4231	6 AX210645	AX210645 Sequence
3	3973.2	99.9	4231	6 AX686744	AX686744 Sequence
4	3973.2	99.9	4231	9 AF071202	AF071202 Homo sapi
5	3968.4	99.8	5759	9 AF081219	AF081219 Homo sapi
6	3966	99.7	6082	6 AR278592	AR278592 Sequence
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18	3965.4	99.7	4515	6 CQ494633	CQ494633 Sequence
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22	3797.8	95.5	6140	6 AR400325	AR400325 Sequence
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35	2323.6	58.4	4878	5 AJ719382	AJ719382 Gallus ga
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37	1892.8	47.6	2143	9 AY133678	AY133678 Homo sapi
38	1892.8	47.6	2256	9 AY133679	AY133679 Homo sapi
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42	1047	26.3	1074	6 AX201051	AX201051 Sequence
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ALIGNMENTS

RESULT 1	AY207008	4004 bp	mrna	linear	PRI 01-JUN-2003
LOCUS	AY207008				
DEFINITION	Homo sapiens ATP-binding cassette transporter C4 (ABCC4) mRNA,				
ACCESSION	AY207008				
VERSION	AY207008.1				
KEYWORDS	GI:31322320				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 4004)				
TITLE	Kato,R. and Ishikawa,T.				
JOURNAL	Direct Submission				
	Submitted (24-DEC-2002) Department of Biomolecular Engineering,				
	Graduate School of Bioscience and Biotechnology, Tokyo Institute of				
	Technology, 4259 Nagatsuda-cho, Midori-ku, Yokohama-shi, Kanagawa				
	226-8501, Japan				
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	PLQIAVATALLWEIGISGLAGNAVLIILLPLQSCFKLPSLSKATATFADIRTM				
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FETAL"

ORIGIN

Query Match	99.9%;	Score	3974.8;	DB	9;	Length	4004;		
Best Local Similarity	99.9%;	Pred.	No. 0;						
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Qy	61	CGCGTGTCTCTCGTGGCTCAATCCCTTGTTHAAANTTGGCCATAACGGAGATTAG	120						
Db	66	CGCGTGTCTCTCGTGGCTCAATCCCTTGTTHAAANTTGGCCATAACGGAGATTAG	125						
Qy	121	GAAGATGATATGATTCAGTGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG	180						
Db	126	GAAGATGATATGATTCAGTGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG	185						
Qy	181	CAAGGGTCTGGGATAAGAAGTTTTAAGAGCTGAGAAATGACGACAGAAAGCCCTCTTTA	240						
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Qy	781	CTGAGGAGTAAAACTGCAACTTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA	840						
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Qy	901	AATTTGAGAAAGAGGAGATTTCAGAGTTCTGAGAAATTCCTGCCTCAGGGGATGAAT	960						
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Qy	1441	CAGCCCTGGGTGTCTCGGAACTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1500						
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LOCUS AX210645 4231 bp DNA linear PAT 31-AUG-2001  
DEFINITION Sequence 287 from Patent WO0157058.  
ACCESSION AX210645  
VERSION AX210645.1 GI:15424905  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Rosenthal,A., Hinzmann,B., Schaefer,R., Zuber,J., Tchernitea,O.,  
Grips,M., Hellriegel,M., Schmitz,A.C. and Sers,C.  
TITLE Detection of differential gene expression  
JOURNAL Patent: WO 0157058-A 287 09-AUG-2001;  
Metagen Gesellschaft fuer Genomforschung mbH (DE)  
FEATURES  
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ORIGIN  
Query Match 99.9%; Score 3973.2; DB 6; Length 4231;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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AUTHORS Eulenbergh, K., Broenner, G., Ciosek, T., Haeder, T. and Steuernagel, A.  
TITLE Protein disulfide isomerase and ABC transporter homologous proteins  
involved in the regulation of energy homeostasis  
JOURNAL Patent: WO 02079238-A 3 10-OCT-2002;  
DeveloGen Aktiengesellschaft fuer Entwicklungsbiologische Forschung  
(DE)

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Qy	601	GATGTGA	CAAGTTTGAT	CAGGTG	CAAGTGT	TTCTTAC	ACTTTC	TGTTGCGGCAGGACCACTG	660	
Db	716	GATGTGA	CAAGTTTGAT	CAGGTG	CAAGTGT	TTCTTAC	ACTTTC	TGTTGCGGCAGGACCACTG	775	
Qy	661	CAGGCAT	TCGACGTG	ACCTACT	CTTGAG	TGGAGAT	GAGAAAT	TATCGTGCCTTGTCTGGG	720	
Db	776	CAGGCAT	TCGACGTG	ACCTACT	CTTGAG	TGGAGAT	GAGAAAT	TATCGTGCCTTGTCTGGG	835	
Qy	721	ATGCGAG	TTCTAA	TCAATCT	CTCTGC	CTTGC	CAAAAG	TGTTTGGGAAGTTGTTCTCATCA	780	
Db	836	ATGCGAG	TTCTAA	TCAATCT	CTCTGC	CTTGC	CAAAAG	TGTTTGGGAAGTTGTTCTCATCA	895	
Qy	781	CTGAGGAG	TAAAC	CTGCAAC	TTTTC	CAGGAT	CCGAGG	ATCAGGACCATGAATGAAGTTATA	840	
Db	896	CTGAGGAG	TAAAC	CTGCAAC	TTTTC	CAGGAT	CCGAGG	ATCAGGACCATGAATGAAGTTATA	955	
Qy	841	ACTGGTA	TAAGCAT	ATAA	TAATAAT	GTAC	CCCTTGGG	AAAGTCATTTTCAAATCTTTATTACC	900	
Db	956	ACTGGTA	TAAGCAT	ATAA	TAATAAT	GTAC	CCCTTGGG	AAAGTCATTTTCAAATCTTTATTACC	1015	
Qy	901	AATTTGAA	AAAGAG	GAGATTT	CCAAG	ATTC	TGAGAA	TGTTCCCTGCATCAGGGGGATGAAT	960	
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1796	DB	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1855
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VERSION AY081219.1 GI:21655122  
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REFERENCE 1 (bases 1 to 5759)  
AUTHORS Adachi,M., Sampath,J., Lan,L.B., Sun,D., Hargrove,P., Flatley,R., Tatum,A., Edwards,M.Z., Wezeman,M., Matherly,L., Drake,R. and Schuetz,J.  
TITLE Expression of MRP4 Confers Resistance to Ganciclovir and Compromises Bystander Cell Killing  
J. Biol. Chem. 277 (41), 38998-39004 (2002)  
JOURNAL  
PUBMED 12105214  
REFERENCE 2 (bases 1 to 5759)  
AUTHORS Adachi,M., Sampath,J., Sun,D. and Schuetz,J.D.  
TITLE Direct Submission  
JOURNAL Submitted (22-FEB-2002) Pharmaceutical Sciences, St. Jude Children's Research Hospital, 332 North Lauderdale St., Memphis, TN 38105-2794, USA  
FEATURES  
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ORIGIN

Query Match		99.8%;	Score 3968.4;	DB 9;	Length 5759;		
Best Local Similarity		99.8%;	Pred. No. 0;				
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QY	61	CGCGTGTCTTCTGGTGCTCAATCCCTGTGTTAAATTTGGCCATAAACCGAGATTAGAG	120				
DB	82	CGCGTGTCTTCTGGTGCTCAATCCCTGTGTTAAATTTGGCCATAAACCGAGATTAGAG	141				
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QY	181	CAAGGGTCTCGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCCCTCTTTA	240				
DB	202	CAAGGGTCTCGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCCCTCTTTA	261				
QY	241	ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA	300				
DB	262	ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA	321				
QY	301	ATTGAGGAAGTGCACAAAGTAAATCCAGCCATATTTTGGGAAATTAATTAATTTT	360				
DB	322	ATTGAGGAAGTGCACAAAGTAAATCCAGCCATATTTTGGGAAATTAATTAATTTT	381				
QY	361	GAATAATATGATCCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCCATGCGACGGTG	420				
DB	382	GAATAATATGATCCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCCATGCGACGGTG	441				
QY	421	CTGACTTTTTCGACGCTCAATTTGGCTATACTGCATCACTTATATTTTATCACGTTTCAG	480				
DB	442	CTGACTTTTTCGACGCTCAATTTGGCTATACTGCATCACTTATATTTTATCACGTTTCAG	501				
QY	481	TGTGCTGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT	540				
DB	502	TGTGCTGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT	561				
QY	541	CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT	600				
DB	562	CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT	621				
QY	601	GATGTGAACAAAGTTTGAATGAGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG	660				
DB	622	GATGTGAACAAAGTTTGAATGAGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG	681				
QY	661	CAGGCGATCGCAGTGAATGCGCTTACTCTGATGAGAGATAGGAATATCGTGCCCTTGTGGG	720				
DB	682	CAGGCGATCGCAGTGAATGCGCTTACTCTGATGAGAGATAGGAATATCGTGCCCTTGTGGG	741				
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QY	841	ACTGGTATAGGATTAATAAATGATAGCTCTGGGAAAGTCAATTTTCAAATCTTATTACC	900				
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Db	922	AATTTGAGAAAGAGGAGATTTTCAAGATTTCTGAGAAAGTTCTCTGCTCAGAGGGATGAAT	981
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LOCUS  
DEFINITION Sequence 535 from patent US 6512094.  
ACCESSION AR278592  
VERSION AR278592.1 GI:29712838  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

AR278592 6082 bp DNA linear PAT 10-APR-2003

REFERENCE 1 (bases 1 to 6082)  
 AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,  
 Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
 Vedick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,  
 Hepler, W.T. and Henderson, R.A.  
 TITLE Compositions and methods for the therapy and diagnosis of prostate  
 cancer  
 JOURNAL Patent: US 6512094-A 535 28-JAN-2003;  
 FEATURES Location/Qualifiers  
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ORIGIN

Query Match 99.7%; Score 3966; DB 6; Length 6082;  
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 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATATGAGGAAGTGAACAA 1920  
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 DEFINITION Sequence 535 from patent US 6329505.  
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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 6082)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yquiu,J.,  
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and  
Day,C.H.  
TITLE Compositions and methods for therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: US 6329505-A 535 11-DEC-2001;  
FEATURES Location/Qualifiers  
source 1..6082  
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ORIGIN

Query Match 99.7%; Score 3966; DB 6; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DEFINITION Sequence 535 from patent US 6620922.  
ACCESSION AR400324  
VERSION AR400324.1 GI:40143590  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6082)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,W., Scolk,J.A., Day,C.H., Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6620922-A 535 16-SEP-2003;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 99.7%; Score 3966; DB 6; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
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VERSION AR405591.1 GI:40154428  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6082)  
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T. and Henderson, R. A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6630305-A 535 07-OCT-2003;  
FEATURES  
source Location/Qualifiers  
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ORIGIN

Query Match 99.7%; Score 3966; DB 6; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 10  
AR563971 AR563971 6082 bp DNA linear PAT 08-OCT-2004  
LOCUS Sequence 535 from patent US 6759515.  
DEFINITION AR563971  
ACCESSION AR563971  
VERSION AR563971.1 GI:53979022  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6082)  
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. F., and Henderson, R. A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6759515-A 535 06-JUL-2004;  
FEATURES Location/Qualifiers  
source 1..6082  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 99.7%; Score 3966; DB 6; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 246 CGCGTGTCTTCTGGGTGCTCAATCCCTTGTGTTTAAATTTGGCCATAAACGGAGATTAGAG 305

Qy 121 GAAGATGATGTTATTCAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGGATTG 180  
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Qy 181 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGAACCTTCTTTA 240  
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Db	2226	AATGCCCAGTTACACTATACAGAGGAGAACCGTCTGAAAGAAAGTTGGTTTTCAGGCC	2285
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Qy	2341	GCAAGATCTCTATTGGTATTCTACGTCTCTGTAACTCTTCACAAACTTTGCAACAA	2400
Db	2526	GCAAGATCTCTATTGGTATTCTACGTCTCTGTAACTCTTCACAAACTTTGCAACAA	2585
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Db	2586	ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTAATCTTTGTATGAAATPCCAATAGGA	2645
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Qy	3301	GATTAAGATCTTGACAACTGAAATTTGGACTTTCACGATTTAAGGAAGAAATGTCATCATATA	3360
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LOCUS Sequence 535 from Patent WO0173032.
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VERSION AX267561.1 GI:16516283
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 535 04-OCT-2001;
CORIXA CORPORATION (US)
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 AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.  
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|
|
Qy 3420 GCACACGGATCAGGAACCTGCGAATGCTTACAGAGGTACAACTTAAGAAACCATTTGA 3479
|
|
|
Db 3519 GCACACGGATCAGGAACCTGCGAATGCTTACAGAGGTACAACTTAAGAAACCATTTGA 3578
|
|
|
Qy 3480 AGATCTTCCTGGTAAATGGGATACCTGAATTAGCAGAACTCAGGATCCAAATTTTAGTGTGG 3539
|
|
|
Db 3579 AGATCTTCCTGGTAAATGGGATACCTGAATTAGCAGAACTCAGGATCCAAATTTTAGTGTGG 3638
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|
|
Qy 3540 ACAAGACAACTGGTGTGCCCTTGGCAGGGCAATTCACAGGAAAAATCAGATATTGATTAT 3599
|
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|
Db 3639 ACAAGACAACTGGTGTGCCCTTGGCAGGGCAATTCACAGGAAAAATCAGATATTGATTAT 3698
|
|
|
Qy 3600 TGATGACGCGACGCAAAATGGATGCTCAAGAACTGATGAGTTAATACAAAAAAATCCG 3659
|
|
|
Db 3699 TGATGACGCGACGCAAAATGGATGCTCAAGAACTGATGAGTTAATACAAAAAAATCCG 3758
|
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|
Qy 3660 GGAGAAATTTGCCCACTGCACCGTCTAAACCAATTGCACACAGATTGAACACCATTTATTGA 3719
|
|
|
Db 3759 GGAGAAATTTGCCCACTGCACCGTCTAAACCAATTGCACACAGATTGAACACCATTTATTGA 3818
|
|
|
Qy 3720 CAGCGACAAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAATATGATGAGCCGTATGT 3779
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|
|
Db 3819 CAGCGACAAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAATATGATGAGCCGTATGT 3878
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|
|
Qy 3780 TTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGA 3839
|
|
|
Db 3879 TTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGA 3938
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|
Qy 3840 AGCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTCCACATAT 3899
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|
Db 3939 AGCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTCCACATAT 3998
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|
|
Qy 3900 TGGTCACACTGACCACACATGGTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTAT 3959
|
|
|
Db 3999 TGGTCACACTGACCACACATGGTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTAT 4058
|
|
|
Qy 3960 TTTGAGACAGCACTGTGA 3978
|
|
|
Db 4059 TTTGAGACAGCACTGTGA 4077
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Search completed: May 20, 2005, 09:10:55  
Job time : 16757 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 19:10:22 ; Search time 1981 Seconds  
(without alignments)  
11887.295 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcctgtgtaccagga.....ttttcagagacgactgtga 3978

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1980s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3978	100.0	3978	6	ABK92135
2	3978	100.0	3978	11	Adn39251 Prostate
3	3974.8	99.9	5271	12	Adh10611 Human can
4	3974.8	99.9	5284	12	Adh10612 Human can
5	3974.8	99.9	5833	12	Adh10624 Human can
6	3974.8	99.9	5862	12	Adh10626 Human can
7	3973.2	99.9	4231	2	Aaz30078 Human dif
8	3973.2	99.9	4231	5	Aah81778 Human dif
9	3973.2	99.9	4231	11	Adn39253 Cancer/an
10	3973.2	99.9	5832	13	Adr66822 Human pro
11	3973.2	99.9	5832	13	Adr65919 Human pro
12	3973.2	99.9	5870	10	Adb75177 Prostate
13	3971.6	99.8	4231	8	Abv75072 Human Dev
14	3966	99.7	6082	4	Aah93828 Human pro
15	3966	99.7	6082	4	Aas63921 Human pro
16	3966	99.7	6082	4	Aah85142 Human pro
17	3966	99.7	6082	5	Acc59729 Prostate
18	3966	99.7	6082	6	Adl95292 Human P51
19	3966	99.7	6082	8	Acc95456 Prostate
20	3966	99.7	6082	10	Adb13985 Human pro

21	3966	99.7	6082	10	ADG26401	Adg26401 Human pro
22	3965.4	99.7	4515	5	ABV24188	Abv24188 Human pro
23	3965.4	99.7	4515	5	ABV26511	Abv26511 Human pro
24	3965.4	99.7	4515	5	ABV20669	Abv20669 Human pro
25	3965.4	99.7	4515	5	ABV22410	Abv22410 Human pro
26	3965.4	99.7	4515	5	ABV24580	Abv24580 Human pro
27	3965.4	99.7	4515	5	ABV28224	Abv28224 Human pro
28	3899	98.0	3913	12	ADQ59423	Adq59423 Human can
29	3797.8	95.5	6140	4	AAH93829	Aah93829 Human pro
30	3797.8	95.5	6140	4	AAH63922	Aas63922 Human pro
31	3797.8	95.5	6140	4	AAH85143	Aah85143 Human pro
32	3797.8	95.5	6140	5	ACA59730	Acc59730 Prostate
33	3797.8	95.5	6140	6	ABL95293	AbL95293 Human P51
34	3797.8	95.5	6140	8	ACC95457	Acc95457 Prostate
35	3797.8	95.5	6140	10	ADB13986	Adb13986 Human pro
36	3797.8	95.5	6140	10	ADG26402	Adg26402 Human pro
37	3742.4	94.1	4395	8	ACC95747	Acc95747 Prostate
38	3742.4	94.1	4395	10	ADB14457	Adb14457 Expressio
39	3742.4	94.1	4395	10	ADG26980	Adg26980 Human pro
40	3741.8	94.1	3786	8	ACC95746	Acc95746 Prostate
41	3741.8	94.1	3786	10	ADB14456	Adb14456 Expressio
42	3741.8	94.1	3786	10	ADG26979	Adg26979 Human pro
43	2802.8	70.5	3521	12	ADH10613	Adh10613 Human can
44	2642.8	66.4	5550	12	ADQ59420	Adq59420 Human can
45	1294.2	32.5	3200	12	ADH10616	Adh10616 Human can

#### ALIGNMENTS

RESULT 1

ABK92135  
ID ABK92135 standard; DNA; 3978 BP.  
XX  
AC ABK92135;  
XX  
DT 15-AUG-2002 (first entry)  
XX  
DE Prostate cancer-associated DNA sequence #21.

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;  
KW gene therapy; gene; ds.  
XX  
OS Mammalia.

XX WO2002030268-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-US032045.

XX 13-OCT-2000; 2000US-00687576.

XX 08-DEC-2000; 2000US-00733288.

XX 24-JAN-2001; 2001US-0263957P.

XX 16-MAR-2001; 2001US-0276791P.

XX 16-MAR-2001; 2001US-0276888P.

XX 06-APR-2001; 2001US-0281922P.

XX 24-APR-2001; 2001US-0286214P.

XX 30-APR-2001; 2001US-00847046.

XX 04-MAY-2001; 2001US-0288589P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevez P;

XX WPI; 2002-471335/50.

XX P-PSDB; ABG61820.

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XX Claim 22; Page 316; 436pp; English.

CC The present invention relates to methods of detecting a prostate cancer-  
 CC associated transcript in a cell from a patient. The method comprises  
 CC contacting a biological sample from the patient with prostate cancer-  
 CC associated polynucleotides (designated pC genes) that selectively  
 CC hybridize to a sequence that is at least 80% identical to them. The  
 CC prostate cancer-associated polynucleotide sequences are differentially  
 CC expressed in prostate tumour tissue or in prostate cancer and are derived  
 CC from the tissues of various organisms such as humans or other mammals  
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
 CC associated genes are useful for diagnosing or treating prostate cancer,  
 CC as well as for identifying modulators of prostate cancer or agents that  
 CC inhibit prostate cancer. The nucleic acid sequences are particularly  
 CC useful in gene therapy, as a vaccine or in antisense applications.  
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide  
 CC sequences

XX SQ Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;

Query Match 100.0%; Score 3978; DB 6; Length 3978;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCCGTTACAGAGAGTGAAGCCCAACCCGCTGCAGGACGGCAACCTCTGCTCA 60  
 Db 1 ATGCTGCCGTTACAGAGAGTGAAGCCCAACCCGCTGCAGGACGGCAACCTCTGCTCA 60

Qy 61 CGCGTGTTCTTCGGTGGCTCAATCCCTGTTTAAATTTGCCATAAAGGAGATTAG 120  
 Db 61 CGCGTGTTCTTCGGTGGCTCAATCCCTGTTTAAATTTGCCATAAAGGAGATTAG 120

Qy 121 GAAGATGATATGATTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180  
 Db 121 GAAGATGATATGATTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180

Qy 181 CAAGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGAGCAAGAGCCCTTCTTTA 240  
 Db 181 CAAGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGAGCAAGAGCCCTTCTTTA 240

Qy 241 ACAGAGCAATCATAAAGTTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
 Db 241 ACAGAGCAATCATAAAGTTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300

Qy 301 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 360  
 Db 301 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 360

Qy 361 GAAATTTATGATCCCATGGATTCGTGGCTTTGAAACACAGGGTACGCTATGCCACGGTG 420  
 Db 361 GAAATTTATGATCCCATGGATTCGTGGCTTTGAAACACAGGGTACGCTATGCCACGGTG 420

Qy 421 CTGACTTTTTCACGCTCATTTTGGCTATCTGCTATCTGCTATATTTTATCAGTTTCAG 480  
 Db 421 CTGACTTTTTCACGCTCATTTTGGCTATCTGCTATCTGCTATATTTTATCAGTTTCAG 480

Qy 481 TGTGCTGGGATGAGGTTACAGTACGCAATGTCATATGATTTATCGAAGGCACTTCGT 540  
 Db 481 TGTGCTGGGATGAGGTTACAGTACGCAATGTCATATGATTTATCGAAGGCACTTCGT 540

Qy 541 CTTAGTAAATGAGGATGGGGAAGACCAACACAGGCCAGATAGTCAATCTGCTGCTCAAT 600  
 Db 541 CTTAGTAAATGAGGATGGGGAAGACCAACACAGGCCAGATAGTCAATCTGCTGCTCAAT 600

Qy 601 GATGTGAACAGTTTGTATCAGTGCAGTGTCTTACACTTCTGCTGGGAGGACCACTG 660  
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Qy 661 CAGGCGATCGAGTACCTGCTTCTGGAATGAGATAGGAATATCGTGCCTTCTGCTGGG 720  
 Db 661 CAGGCGATCGAGTACCTGCTTCTGGAATGAGATAGGAATATCGTGCCTTCTGCTGGG 720

721 ATGCGAGTCTTAATCATTCTCCTGCCCTTGCAGAGCTGTTTGGGAGTTGTTCTCATCA 780  
 Db 721 ATGCGAGTCTTAATCATTCTCCTGCCCTTGCAGAGCTGTTTGGGAGTTGTTCTCATCA 780

781 CTGAGGAGTAAACTGCAACTTTTCACGATGCGAGGATCAGGACCATGAATGAAGTTATA 840  
 Db 781 CTGAGGAGTAAACTGCAACTTTTCACGATGCGAGGATCAGGACCATGAATGAAGTTATA 840

841 ACTGGTATAAGGATAATAAAATGTACGCTGGGAAAAGTCAATTTTCAAAATCTTATTAAC 900  
 Db 841 ACTGGTATAAGGATAATAAAATGTACGCTGGGAAAAGTCAATTTTCAAAATCTTATTAAC 900

901 AATTGGAAGAAGGAGATTTCAGAGTTCTGAGAGTTCTGCTCCCTCAGGGGATGAAT 960  
 Db 901 AATTGGAAGAAGGAGATTTCAGAGTTCTGAGAGTTCTGCTCCCTCAGGGGATGAAT 960

961 TTGGCTTCGTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCACCACCTAGCTG 1020  
 Db 961 TTGGCTTCGTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCACCACCTAGCTG 1020

1021 CTCTCGGCAAGTGTGATCACAGCCAGCCGCTGTTCTGTCAGTGACGCTGTATGGGGCT 1080  
 Db 1021 CTCTCGGCAAGTGTGATCACAGCCAGCCGCTGTTCTGTCAGTGACGCTGTATGGGGCT 1080

1081 GTGGGCTGACGTTTACCTCTTCTTCCCTCAGCCATTGAGGGGTGTGAGAGGCAATC 1140  
 Db 1081 GTGGGCTGACGTTTACCTCTTCTTCCCTCAGCCATTGAGGGGTGTGAGAGGCAATC 1140

1141 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTTGTGATGAGATATCACAGCGCAACCGT 1200  
 Db 1141 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTTGTGATGAGATATCACAGCGCAACCGT 1200

1201 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGTCAGGATTTTACTGCTTTTGGGAT 1260  
 Db 1201 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGTCAGGATTTTACTGCTTTTGGGAT 1260

1261 AAGGCATCAGAGACCCCACTCTACAGGCTTTTCTTTACTGTCAGACCTGGGGAATTG 1320  
 Db 1261 AAGGCATCAGAGACCCCACTCTACAGGCTTTTCTTTTACTGTCAGACCTGGGGAATTG 1320

1321 TTAGCTGTGCTCGGCCCGCTGGGAGAGGAAAGTCACTGTTTAAAGTGGCGCTCTCGGG 1380  
 Db 1321 TTAGCTGTGCTCGGCCCGCTGGGAGAGGAAAGTCACTGTTTAAAGTGGCGCTCTCGGG 1380

1381 GAATGTCGCCCAAGTCAACGGCTGCTCAGCGTGATGGAAGATTTGCTATGTCCTCAG 1440  
 Db 1381 GAATGTCGCCCAAGTCAACGGCTGCTCAGCGTGATGGAAGATTTGCTATGTCCTCAG 1440

1441 CAGCCCTGGGCTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
 Db 1441 CAGCCCTGGGCTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500

1501 AAGGAACGATATGAAAAAGTCAATAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTG 1560  
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1561 GAGGATGGTATCTGACTGTGATAGGAGATCGGGGAACCAACGCTGAGTGAGGGGAGAAA 1620  
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 Db 1621 GCAGGGTAAACCTTGCAGAGGAGTGTATCAGATGCTGACATCTATCTCTCGACGAT 1680

1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
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1741 ATTTTGCATGAGAAAGATCAAAATTTTATGATGATCATCAGTTTGCAGTACCTCAAGAGCTGCA 1800  
 Db 1741 ATTTTGCATGAGAAAGATCAAAATTTTATGATGATCATCAGTTTGCAGTACCTCAAGAGCTGCA 1800

QY 1801 AGTCAGATCTTGATATTGAAAGATGGTAAATGGTGAGAGGGGACTTACACTGAGTTC 1860  
DB 1801 AGTCAGATCTTGATATTGAAAGATGGTAAATGGTGAGAGGGGACTTACACTGAGTTC 1860  
QY 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAACAA 1920  
DB 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAACAA 1920  
QY 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACTCTCTCAGAGTCTTCCGTTTGG 1980  
DB 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACTCTCTCAGAGTCTTCCGTTTGG 1980  
QY 1981 TCTCAACAACTCTCAGACCTCTCTGAAAGATGGTCTCTGAGAGCCCAAGATACAGAG 2040  
DB 1981 TCTCAACAACTCTCAGACCTCTCTGAAAGATGGTCTCTGAGAGCCCAAGATACAGAG 2040  
QY 2041 AATGTCAGGTACACTATCAGAGAGAAACCGTTCTGAGGAAAGTGGTTTTCAGGCC 2100  
DB 2041 AATGTCAGGTACACTATCAGAGAGAAACCGTTCTGAGGAAAGTGGTTTTCAGGCC 2100  
QY 2101 TATAAGAAATTACTTTCAGAGCTGGTCTCACTGGATGTCCTCATTTTCTTATTTCTCCTA 2160  
DB 2101 TATAAGAAATTACTTTCAGAGCTGGTCTCACTGGATGTCCTCATTTTCTTATTTCTCCTA 2160  
QY 2161 AACACTGCAGCTCAGGTTGCCATATGTCTTCAAGATTGGTGGCTTTCATACTGGGCAAC 2220  
DB 2161 AACACTGCAGCTCAGGTTGCCATATGTCTTCAAGATTGGTGGCTTTCATACTGGGCAAC 2220  
QY 2221 AACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAAACGAGAGCTAGAT 2280  
DB 2221 AACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAAACGAGAGCTAGAT 2280  
QY 2281 CTTAACTGGTACTTACGAAATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 2340  
DB 2281 CTTAACTGGTACTTACGAAATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 2340  
QY 2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTAACTCTTCAACAACTTTGCAACAA 2400  
DB 2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTAACTCTTCAACAACTTTGCAACAA 2400  
QY 2401 ATGTTGAGTCAATCTGAAAGCTCCGGTATATTCTTTGATAGAAATCCAAATAGGAAGA 2460  
DB 2401 ATGTTTGAATCAATCTGAAAGCTCCGGTATATTCTTTGATAGAAATCCAAATAGGAAGA 2460  
QY 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGACACTTGGATGATTTGCTGCGCTGACGTTT 2520  
DB 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGACACTTGGATGATTTGCTGCGCTGACGTTT 2520  
QY 2521 TTAGATTTCTACAGACATTTGCTACAAAGTGGTGGTGGTCTCTGCTGGCTGTGGCCGTG 2580  
DB 2521 TTAGATTTCTACAGACATTTGCTACAAAGTGGTGGTGGTCTCTGCTGGCTGTGGCCGTG 2580  
QY 2581 ATTCTTTGGATCGCAATACCCCTTGGTTCCCTTTGGAAATCAATTTTCAATTTTCTCGGCGA 2640  
DB 2581 ATTCTTTGGATCGCAATACCCCTTGGTTCCCTTTGGAAATCAATTTTCAATTTTCTCGGCGA 2640  
QY 2641 TATTTTGGAAAGTCAAGAGATGTGAAGCGCTGGAATCTCAATCTCGAGTCCAGTG 2700  
DB 2641 TATTTTGGAAAGTCAAGAGATGTGAAGCGCTGGAATCTCAATCTCGAGTCCAGTG 2700  
QY 2701 TTTTCCCACTTGTCTCTCTCCAGGGCTCTGGACCAATCCGGGCAATACAAAGCAGAA 2760  
DB 2701 TTTTCCCACTTGTCTCTCTCCAGGGCTCTGGACCAATCCGGGCAATACAAAGCAGAA 2760  
QY 2761 GAGAGGTGTCAGGAACTGTTTGTATGACACCAAGGATTTAATTCAGAGGCTTGGTTCTTG 2820  
DB 2761 GAGAGGTGTCAGGAACTGTTTGTATGACACCAAGGATTTAATTCAGAGGCTTGGTTCTTG 2820  
QY 2821 TTTTGTGACAGCTCCCGCTGGTTCGGCTCGGTCTGATGTCATCTGTGCAATGTTTGTG 2880  
DB 2821 TTTTGTGACAGCTCCCGCTGGTTCGGCTCGGTCTGATGTCATCTGTGCAATGTTTGTG 2880  
QY 2881 ATCATCGTTGGCTTCTGGTCCCTGATTTCTGCAAAAACTCTGGATCGCGGAGGTTGGT 2940

DB 2881 ATCATCGTTGGCTTCTGGTCCCTGATTTCTGCAAAAACTCTGGATCGCGGAGGTTGGT 2940  
QY 2941 TTGGCACTGTCTTATGCTTCCCTCAGCTCATGGGGATGTTTCACTGGTGTGTTTCGACAAAGT 3000  
DB 2941 TTGGCACTGTCTTATGCTTCCCTCAGCTCATGGGGATGTTTCACTGGTGTGTTTCGACAAAGT 3000  
QY 3001 GCTGAAGTTCAGAAATATGATGATCTCAGTAGAAGAGGTCTATTGAATACACAGACTTGAA 3060  
DB 3001 GCTGAAGTTCAGAAATATGATGATCTCAGTAGAAGAGGTCTATTGAATACACAGACTTGAA 3060  
QY 3061 AAAGAAGCACTTTGGGAATATCAGAAACGCCACCAACAGCTCGCCCCCATGAAAGGAGTG 3120  
DB 3061 AAAGAAGCACTTTGGGAATATCAGAAACGCCACCAACAGCTCGCCCCCATGAAAGGAGTG 3120  
QY 3121 ATAATCTTTGCAATGTGAACCTTCACTGACAGTCCAGGTGGGCTCTGTTACTGAAGCAT 3180  
DB 3121 ATAATCTTTGCAATGTGAACCTTCACTGACAGTCCAGGTGGGCTCTGTTACTGAAGCAT 3180  
QY 3181 CTGACAGCACTCATTTAAATCAAGAAAGGTTGGCATTTGGGAAAGAACCGGAGCTGGA 3240  
DB 3181 CTGACAGCACTCATTTAAATCAAGAAAGGTTGGCATTTGGGAAAGAACCGGAGCTGGA 3240  
QY 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTGTAGATTTGTGAGAACCCGAGGTAAATTTGGATT 3300  
DB 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTGTAGATTTGTGAGAACCCGAGGTAAATTTGGATT 3300  
QY 3301 GATAAGATCTTGCACTGAAATTTGGACTTCAAGATTTAAGGAAGAAATGTCAATCAT 3360  
DB 3301 GATAAGATCTTGCACTGAAATTTGGACTTCAAGATTTAAGGAAGAAATGTCAATCAT 3360  
QY 3361 CCTCAGGAACTGTGTTTGTCTCAGTGAACCAATGAGGAAACCTTGGATCCCTTTAATGAG 3420  
DB 3361 CCTCAGGAACTGTGTTTGTCTCAGTGAACCAATGAGGAAACCTTGGATCCCTTTAATGAG 3420  
QY 3421 CACAAGGATGAGAACTGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCATTTGAA 3480  
DB 3421 CACAAGGATGAGAACTGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCATTTGAA 3480  
QY 3481 GATCTTCTGTTAAATGGATCTGAATTTAGCAGAACTCAGATCCCAATTTTAGTGTGGA 3540  
DB 3481 GATCTTCTGTTAAATGGATCTGAATTTAGCAGAACTCAGATCCCAATTTTAGTGTGGA 3540  
QY 3541 CAAAGCAACTGTGTGCTTGGCCCTGAGGGCAATCTCAGGAAATCAGATATTCATTTATT 3600  
DB 3541 CAAAGCAACTGTGTGCTTGGCCCTGAGGGCAATCTCAGGAAATCAGATATTCATTTATT 3600  
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DB 3601 GATGAAGCGACGGCAATGTGGATCCAAAGAACTGATGAGTTAAATACAAAAAATCCGG 3660  
QY 3661 GAGAAATTTGCCCACTGACCGTCTAACCATTTGACACACAGATTTGAACACCATTTTAC 3720  
DB 3661 GAGAAATTTGCCCACTGACCGTCTAACCATTTGACACACAGATTTGAACACCATTTTAC 3720  
QY 3721 AGGCAAGGATAATGTTTGTAGATTTAGGAAAGTGAAGAAATATGATGAGCCGTATGTT 3780  
DB 3721 AGGCAAGGATAATGTTTGTAGATTTAGGAAAGTGAAGAAATATGATGAGCCGTATGTT 3780  
QY 3781 TTGCTGCAAAATTAAGAGAGCTTATTTTACAAGATGTTGCAACAACTGGGCAAGGAGAA 3840  
DB 3781 TTGCTGCAAAATTAAGAGAGCTTATTTTACAAGATGTTGCAACAACTGGGCAAGGAGAA 3840  
QY 3841 GCCGCTGCCCTCATCTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATTT 3900  
DB 3841 GCCGCTGCCCTCATCTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATTT 3900  
QY 3901 GGTTCACACTGACACATGGTTTACAACACTTCCAAATGAGACAGCCCTCGACCTTAACATTT 3960  
DB 3901 GGTTCACACTGACACATGGTTTACAACACTTCCAAATGAGACAGCCCTCGACCTTAACATTT 3960  
QY 3961 TTGAGACAGCACTGTGA 3978



Qy	901	AATTTGAAAGAAAGGAGATTTCAAGATTCGAAAGTTCCTGCCCTCAGGGGATGAAT	960
Db	901	AAATTTGAAAGAAAGGAGATTTCAAGATTCGAAAGTTCCTGCCCTCAGGGGATGAAT	960
Qy	961	TTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTTTGTGACCTTCACCACTACGTG	1020
Db	961	TTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTTTGTGACCTTCACCACTACGTG	1020
Qy	1021	CTCCTCGGCAGTGTGATCACAGCCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGCT	1080
Db	1021	CTCCTCGGCAGTGTGATCACAGCCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGCT	1080
Qy	1081	GTGGGTGACGGTTACCCCTCTTCCCTCAGCCATTCAGAGGGTGTTCAGAGGCAATC	1140
Db	1081	GTGGGTGACGGTTACCCCTCTTCCCTCAGCCATTCAGAGGGTGTTCAGAGGCAATC	1140
Qy	1141	GTGAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGTGATGAGATATCACAGCGCAACGT	1200
Db	1141	GTGAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGTGATGAGATATCACAGCGCAACGT	1200
Qy	1201	CAGCTGCCGTGAGATGTTAAAGATGCTGATGTCAGGATTTTACTGCTTTTGGAT	1260
Db	1201	CAGCTGCCGTGAGATGTTAAAGATGCTGATGTCAGGATTTTACTGCTTTTGGAT	1260
Qy	1261	AAGCATCAGAGACCCCAACTCTACAAGGCCCTTTCTTTACTGTACAGACCTGGCAGATTG	1320
Db	1261	AAGCATCAGAGACCCCAACTCTACAAGGCCCTTTCTTTACTGTACAGACCTGGCAGATTG	1320
Qy	1321	TTAGCTGTGTCGCCCGCTGGAGCAGGAGTCATCATCTGTTAAGTGCCTCGG	1380
Db	1321	TTAGCTGTGTCGCCCGCTGGAGCAGGAGTCATCATCTGTTAAGTGCCTCGG	1380
Qy	1381	GAATTTGCCCAAGTCACGGGCTGTCAGCGTGATGAGAAATGCTATGCTCTCAG	1440
Db	1381	GAATTTGCCCAAGTCACGGGCTGTCAGCGTGATGAGAAATGCTATGCTCTCAG	1440
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCAGGAGTAAATATTTTATTTGGGAAGAAATACGAA	1500
Db	1441	CAGCCCTGGGTGTTCTCGGGAACCTCAGGAGTAAATATTTTATTTGGGAAGAAATACGAA	1500
Qy	1501	AAGGAACGATATGAAAAGTCATAAAGGCTTGTCTCTGAAAAGGATTTACAGCTGTG	1560
Db	1501	AAGGAACGATATGAAAAGTCATAAAGGCTTGTCTCTGAAAAGGATTTACAGCTGTG	1560
Qy	1561	GAGATGCTGATCTGATGATAGGAGATCGGGGAACCGCTGAGTGGAGGSCAGAAA	1620
Db	1561	GAGATGCTGATCTGATGATAGGAGATCGGGGAACCGCTGAGTGGAGGSCAGAAA	1620
Qy	1621	GCACGGGTAAACCTTTGCAAGACAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT	1680
Db	1621	GCACGGGTAAACCTTTGCAAGACAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT	1680
Qy	1681	CCTCTCAGTGAGATGCGGAAGTTAGCAGACACCTTTGTCGAACCTGTGTATTTGTCAA	1740
Db	1681	CCTCTCAGTGAGATGCGGAAGTTAGCAGACACCTTTGTCGAACCTGTGTATTTGTCAA	1740
Qy	1741	ATTTTGATGAGAGATCACAAATTTTGTGATCTCATCAGTTGTCAGTACCTCAAGCTGCA	1800
Db	1741	ATTTTGATGAGAGATCACAAATTTTGTGATCTCATCAGTTGTCAGTACCTCAAGCTGCA	1800
Qy	1801	AGTCAGATTTCTGATATTTGAAAGATGTTAAATGTCAGAGGGGACTTACACTGAGTTC	1860
Db	1801	AGTCAGATTTCTGATATTTGAAAGATGTTAAATGTCAGAGGGGACTTACACTGAGTTC	1860
Qy	1861	CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATGAGGAAGTGAACAA	1920
Db	1861	CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATGAGGAAGTGAACAA	1920
Qy	1921	CCTCCAGTCCAGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG	1980
Db	1921	CCTCCAGTCCAGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG	1980
Qy	1981	TCTCAACAAATCTCTAGACCCCTCTTGAAGATGGTGTCTCTGGAGAGCAGATACAGAG	2040

Db	1981	TCTCAACAAATCTCTAGACCCCTCTTGAAGATGGTGTCTCTGGAGAGCAGATACAGAG	2040
Qy	2041	AAATGCCAGTTACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC	2100
Db	2041	AAATGCCAGTTACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC	2100
Qy	2101	TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGATTGTCTTCAATTTCTCTTATTCCTA	2160
Db	2101	TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGATTGTCTTCAATTTCTCTTATTCCTA	2160
Qy	2161	AACACTGCAGTCAAGTTGCTTCAAGATTGGTGGCTTTCATATCTGGGCAAAAC	2220
Db	2161	AACACTGCAGTCAAGTTGCTTCAAGATTGGTGGCTTTCATATCTGGGCAAAAC	2220
Qy	2221	AAACAAAGTATGCTAAATGTCACTGTAATGAGGAGGAAATGTAACCGGAGAGCTAGAT	2280
Db	2221	AAACAAAGTATGCTAAATGTCACTGTAATGAGGAGGAAATGTAACCGGAGAGCTAGAT	2280
Qy	2281	CTTAACTGGTACTTAGGAAATTTAATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Db	2281	CTTAACTGGTACTTAGGAAATTTAATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Qy	2341	GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTCAAAAACCTTTGCACAACAAA	2400
Db	2341	GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTCAAAAACCTTTGCACAACAAA	2400
Qy	2401	ATGTTTCAGTCAATTCGAAAGCTCCGGTATTTCTTGTATAGAAATCCAATAGGAAGA	2460
Db	2401	ATGTTTCAGTCAATTCGAAAGCTCCGGTATTTCTTGTATAGAAATCCAATAGGAAGA	2460
Qy	2461	ATTTAAATCGTTTCTCCAAAGACATTTGGACATTTGGATGATTTGCTGCCCTCAGCTTT	2520
Db	2461	ATTTAAATCGTTTCTCCAAAGACATTTGGACATTTGGATGATTTGCTGCCCTCAGCTTT	2520
Qy	2521	TTAGATTTCAATCCAGACATTTGCTCAAGTGGTGGTGGTGTCTCTGGGCTGTGGCCCTG	2580
Db	2521	TTAGATTTCAATCCAGACATTTGCTCAAGTGGTGGTGGTGTCTCTGGGCTGTGGCCCTG	2580
Qy	2581	ATTCCTTGGATCCCAATACCTTGGTTCCCTTGGGAATCATTTTCATTTTCTTCGGCGA	2640
Db	2581	ATTCCTTGGATCCCAATACCTTGGTTCCCTTGGGAATCATTTTCATTTTCTTCGGCGA	2640
Qy	2641	TATTTTGGAAACGCTCAAGAGATGTGAAGCGCTCGAATCTACAACTCGGAGTCCAGTG	2700
Db	2641	TATTTTGGAAACGCTCAAGAGATGTGAAGCGCTCGAATCTACAACTCGGAGTCCAGTG	2700
Qy	2701	TTTTCCCACTTGTCACTTCTCTCCAGGGGCTCTGGACCAATCCGGGCATACAAAGCAGAA	2760
Db	2701	TTTTCCCACTTGTCACTTCTCTCCAGGGGCTCTGGACCAATCCGGGCATACAAAGCAGAA	2760
Qy	2761	GAGAGGTTCAGGAACTGTTTGTATGACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	2820
Db	2761	GAGAGGTTCAGGAACTGTTTGTATGACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	2820
Qy	2821	TTTTTGACAAAGCTCCCGCTGCTCGCGTCTGATGCGCATCTGTGCCATGTGTTGTC	2880
Db	2821	TTTTTGACAAAGCTCCCGCTGCTCGCGTCTGATGCGCATCTGTGCCATGTGTTGTC	2880
Qy	2881	ATCATCTGCTTGGGTCCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT	2940
Db	2881	ATCATCTGCTTGGGTCCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT	2940
Qy	2941	TTGGCAGTCTCTATGCGCTCACGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3000
Db	2941	TTGGCAGTCTCTATGCGCTCACGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3000
Qy	3001	GCTGAAGTTCAGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTCAA	3060
Db	3001	GCTGAAGTTCAGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTCAA	3060
Qy	3061	AAAGAACACCTTTGGGAATATCAGAAACGCCCAACACACAGCTCGCCCCCATGAAGGATG	3120
Db	3061	AAAGAACACCTTTGGGAATATCAGAAACGCCCAACACACAGCTCGCCCCCATGAAGGATG	3120

Db 3061 AAGAAGCACCTTGGGAATATCAGAAAGCCACCACAGCCTTGGCCCCCATGAAGGAGTG 3120  
Qy 3121 ATAATCTTTGACAAATGGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3180  
Db 3121 ATAATCTTTGACAAATGGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3180  
Qy 3181 CTGACAGCACTCATTAATACAGAAAGAGTGTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
Db 3181 CTGACAGCACTCATTAATACAGAAAGAGTGTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATGTGAGAACCCGAGGTAAATTTGGATT 3300  
Db 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATGTGAGAACCCGAGGTAAATTTGGATT 3300  
Qy 3301 GATAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCAT 3360  
Db 3301 GATAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCAT 3360  
Qy 3361 CCTCAGCAACTGTTTGTTCACCTGGAAACATAGAGAAACCTGGATCCCTTTAATGAG 3420  
Db 3361 CCTCAGCAACTGTTTGTTCACCTGGAAACATAGAGAAACCTGGATCCCTTTAATGAG 3420  
Qy 3421 CACACGGATGAGGAACCTGTGGAATGCTCTTAACAGAGGTACAACTTAAAGAAACCATTTGAA 3480  
Db 3421 CACACGGATGAGGAACCTGTGGAATGCTCTTAACAGAGGTACAACTTAAAGAAACCATTTGAA 3480  
Qy 3481 GATCTTCTGTTAAATGGATACATGAATAGCAGAAATCAGGATCCAAATTTAGTGTGGA 3540  
Db 3481 GATCTTCTGTTAAATGGATACATGAATAGCAGAAATCAGGATCCAAATTTAGTGTGGA 3540  
Qy 3541 CAAAGCAACTGTGTGCTTGCCTGACGGCAATCTCAGGAAATCAGATATTCATATT 3600  
Db 3541 CAAAGCAACTGTGTGCTTGCCTGACGGCAATCTCAGGAAATCAGATATTCATATT 3600  
Qy 3601 GATGAAGCGACGGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAGAAATCCGG 3660  
Db 3601 GATGAAGCGACGGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAGAAATCCGG 3660  
Qy 3661 GAGAAATTTGCCACTGACCGTCTAACCTTGCACAGATTTGAACACCATTTATTGAC 3720  
Db 3661 GAGAAATTTGCCACTGACCGTCTAACCTTGCACAGATTTGAACACCATTTATTGAC 3720  
Qy 3721 AGGCACAGATAATGGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGACCGTATGTT 3780  
Db 3721 AGGCACAGATAATGGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGACCGTATGTT 3780  
Qy 3781 TTGCTGCAAAATAAAGAGAGCCTATTTTACAGATGGTGCACAACTGGGCAAGGCAGAA 3840  
Db 3781 TTGCTGCAAAATAAAGAGAGCCTATTTTACAGATGGTGCACAACTGGGCAAGGCAGAA 3840  
Qy 3841 GCCGCTGCCCTCACTGAAACAGCAACAGGTATACCTTCAAGAAATTTATCCACATATT 3900  
Db 3841 GCCGCTGCCCTCACTGAAACAGCAACAGGTATACCTTCAAGAAATTTATCCACATATT 3900  
Qy 3901 GGTCACTGACCACTGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 3960  
Db 3901 GGTCACTGACCACTGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 3960  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 3961 TTCGAGACAGCACTGTGA 3978

RESULT 3  
ADH10611  
ID ADH10611 standard; DNA; 5271 BP.  
XX  
AC ADH10611;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human cancer-related polynucleotide, SEQ ID 1.  
XX

KW Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
XX Homo sapiens.  
OS WO2003104404-A2.  
PN 18-DEC-2003.  
PD 05-JUN-2003; 2003WO-US017772.  
PF 06-JUN-2002; 2002US-0386651P.  
PR (AVAL-) AVALON PHARM INC.  
PX Ebner R;  
PI WPI; 2004-062332/06.  
DR Identifying agents that modulate the activity of cancer-related gene,  
XX useful for treating or diagnosing prostate cancer comprising contacting a  
XX compound with a cell containing a gene under conditions promoting a  
XX expression of the gene.  
XX Claim 1; SEQ ID NO 1; 79pp; English.  
XX The invention relates to identifying an agent that modulates the activity  
XX of a cancer-related gene. The method involves contacting a compound with  
XX a cell containing a gene that corresponds to a polynucleotide having a  
XX sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
XX expression of the gene. The method is useful for identifying an agent  
XX that modulates the activity of a cancer-related gene. The polypeptides  
XX and antibodies of the invention are useful for treating and diagnosing  
XX cancer, preferably prostate cancer. It is also useful for screening  
XX assays for agents that are effective in reducing the activity of cancer-  
XX related genes. The present sequence represents a specific example of a  
XX cancer-related polynucleotide sequence.  
SQ Sequence 5271 BP; 1480 A; 1087 C; 1212 G; 1492 T; 0 U; 0 Other;

Query Match 99.9%; Score 3974.8; DB 12; Length 5271;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGCTGCCCTGTACAGGAGGTCAACGCCCTGCGAGGACGCACTCTGCTCA 60  
Db 116 ATGCTGCCCTGTACAGGAGGTCAACGCCCTGCGAGGACGCACTCTGCTCA 175  
Qy 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTAAAAATTGGCCATAAACGGAGATTAG 120  
Db 176 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTAAAAATTGGCCATAAACGGAGATTAG 235  
Qy 121 GAGATGATATGATTTCAGTGTCCGAGAGACCGCTCAGACACCTTGGAGAGGTTG 180  
Db 236 GAGATGATATGATTTCAGTGTCCGAGAGACCGCTCAGACACCTTGGAGAGGTTG 295  
Qy 181 CAAGGGTCTCGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCCTTCTTTA 240  
Db 296 CAAGGGTCTCGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCCTTCTTTA 355  
Qy 241 ACAAGACAATCATAAAGTGTCTCTGGAATCTTATTTAGTTTTGGGAATTTTACGTTA 300  
Db 356 ACAAGACAATCATAAAGTGTCTCTGGAATCTTATTTAGTTTTGGGAATTTTACGTTA 415  
Qy 301 ATTGAGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATATTAATTAATTT 360  
Db 416 ATTGAGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATATTAATTAATTT 475  
Qy 361 GAAAAATTATGATCCCATGGATTCTGTGCTTTTGAACACAGCGTACGCTATGCCACGGTG 420  
Db 476 GAAAAATTATGATCCCATGGATTCTGTGCTTTTGAACACAGCGTACGCTATGCCACGGTG 535  
Qy 421 CTGACTTTTTCGACGCTCAITTTTGGCTATATCTGCATCACTTATATTTTATCAGTTTCA 480

Db	536	CTGACTTTTTGCAAGCTCAATTTTGGCTATACCTGCAATCACTATATATTTTTATCAAGTTCAAG	595
Qy	481	TGTGCTGGGATGAGTTACGATGAGCTAGCCATGTCATATGATTTATCGGAAGCACTTCGT	540
Db	596	TGTGCTGGGATGAGTTACGATGAGCTAGCCATGTCATATGATTTATCGGAAGCACTTCGT	655
Qy	541	CTTAGTAACATGGGCATGGGGAAGAACCAACACAGGCCAGATAGTCAATCTGCTGTCCAAT	600
Db	656	CTTAGTAACATGGGCATGGGGAAGAACCAACACAGGCCAGATAGTCAATCTGCTGTCCAAT	715
Qy	601	GATCTGACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGCTGGGACAGGACCACTG	660
Db	716	GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGCTGGGACAGGACCACTG	775
Qy	661	CAGGCCATCGCAGTGAATGCGCCCTACTCTGGATGGAGATAGGAATATCGTGGCTTCTGGG	720
Db	776	CAGGCCATCGCAGTGAATGCGCCCTACTCTGGATGGAGATAGGAATATCGTGGCTTCTGGG	835
Qy	721	ATGGCAGTCTTAATCAATCTCTGCTGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCT	780
Db	836	ATGGCAGTCTTAATCAATCTCTGCTGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCT	895
Qy	781	CTGAGGATTAACATGCACTTCTACCGGATCCAGGATCAGGACATGAATGAAGTTATA	840
Db	896	CTGAGGATTAACATGCACTTCTACCGGATCCAGGATCAGGACATGAATGAAGTTATA	955
Qy	841	ACTGGTATAAGGATAATAAATAATGACGCTCGGGAAGTCAATTTCAAATCTTTATTACC	900
Db	956	ACTGGTATAAGGATAATAAATAATGACGCTCGGGAAGTCAATTTCAAATCTTTATTACC	1015
Qy	901	AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAATCTCTGCTCAGGGGATGAAT	960
Db	1016	AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAATCTCTGCTCAGGGGATGAAT	1075
Qy	961	TTGGCTTCTGTTTTCAGTGCAGCAAAATCATCTGTTTGTGACCTTTCACCACTACGTTG	1020
Db	1076	TTGGCTTCTGTTTTCAGTGCAGCAAAATCATCTGTTTGTGACCTTTCACCACTACGTTG	1135
Qy	1021	CTCCTCGGCTGATGATCAGCAGCAGCGCGTGTCTGTTGGCAGTGACGCTGATGGGGCT	1080
Db	1136	CTCCTCGGCTGATGATCAGCAGCAGCGCGTGTCTGTTGGCAGTGACGCTGATGGGGCT	1195
Qy	1081	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC	1140
Db	1196	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC	1255
Qy	1141	GTGAGCATCCGAGAAATCCAGACCTTTTGTGCTACTTGATGAGATATCAAGCGCAACCGT	1200
Db	1256	GTGAGCATCCGAGAAATCCAGACCTTTTGTGCTACTTGATGAGATATCAAGCGCAACCGT	1315
Qy	1201	CAGCTGCGCTCAGATGTTAAAGATGTTGATGATGATGATGATGATGATGATGATGATGAT	1260
Db	1316	CAGCTGCGCTCAGATGTTAAAGATGTTGATGATGATGATGATGATGATGATGATGATGAT	1375
Qy	1261	AAGGCATCAGAGACCCCACTCTCAAGGCTTTTCTTTTCTGTCAGACCTGGGGAATTG	1320
Db	1376	AAGGCATCAGAGACCCCACTCTCAAGGCTTTTCTTTTCTGTCAGACCTGGGGAATTG	1435
Qy	1321	TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTTAAAGTGCCTGCTCGG	1380
Db	1436	TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTTAAAGTGCCTGCTCGG	1495
Qy	1381	GAATTTGCCCAAGTCAAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT	1440
Db	1496	GAATTTGCCCAAGTCAAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT	1555
Qy	1441	CAGCCCTGGGTGTTCTCGGGAATCTGAGGAGTAAATTTTTTATTTGGGAAGAAATACGAA	1500
Db	1556	CAGCCCTGGGTGTTCTCGGGAATCTGAGGAGTAAATTTTTTATTTGGGAAGAAATACGAA	1615
Qy	1501	AAGGAAAGATATAAAGTCAATAAGCTTGTCTCTGAAAAAGGATTTTACAGCTGTG	1560
Db	1616	AAGGAAAGATATAAAGTCAATAAGCTTGTCTCTGAAAAAGGATTTTACAGCTGTG	1675
Qy	1561	GAGGATGCTGATCTGACTGTGATAGGAGATCGGGAAACCAAGCTCAGTGGAGGCGAGAAA	1620
Db	1676	GAGGATGCTGATCTGACTGTGATAGGAGATCGGGAAACCAAGCTCAGTGGAGGCGAGAAA	1735
Qy	1621	GCACGGGTAAACCTTTGCAAGAGCAGTGTATCAAGATGCTGACATCTCTCTGAGCAAT	1680
Db	1736	GCACGGGTAAACCTTTGCAAGAGCAGTGTATCAAGATGCTGACATCTCTCTGAGCAAT	1795
Qy	1681	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAA	1740
Db	1796	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAA	1855
Qy	1741	ATTTTGATGAGAGAGATCACAATTTTGTAGTGAATCATCAGTTGTCAGTACTCTCAAGCTGCA	1800
Db	1856	ATTTTGATGAGAGAGATCACAATTTTGTAGTGAATCATCAGTTGTCAGTACTCTCAAGCTGCA	1915
Qy	1801	AGTCAGATTTCTGATATTTGAAAGATGTTAAATGTTGCAAGAGGGAATTAACACTGAGTTC	1860
Db	1916	AGTCAGATTTCTGATATTTGAAAGATGTTAAATGTTGCAAGAGGGAATTTACACTGAGTTC	1975
Qy	1861	CTAAAACTCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATAATGAGGAAGTGAACAA	1920
Db	1976	CTAAAACTCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATAATGAGGAAGTGAACAA	2035
Qy	1921	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACTTCTCAGAGTCTTTCGGTTTGG	1980
Db	2036	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACTTCTCAGAGTCTTTCGGTTTGG	2095
Qy	1981	TCTCAACAATCTTCTAGACCTCTTGAAGATGGTGTCTGAGAGCAGCAAGATACAGAG	2040
Db	2096	TCTCAACAATCTTCTAGACCTCTTGAAGATGGTGTCTGAGAGCAGCAAGATACAGAG	2155
Qy	2041	AATGTCAGGTTTACACTATCAGAGGAAACCGTTCTGAAGAAAGTGGTTTTCAGGCC	2100
Db	2156	AATGTCAGGTTTACACTATCAGAGGAAACCGTTCTGAAGAAAGTGGTTTTCAGGCC	2215
Qy	2101	TATAAGAAATTTACTTTCAGAGCTGGTGTCTCACTGGAATGTCTTCAATTTTCTTATCTCCTA	2160
Db	2216	TATAAGAAATTTACTTTCAGAGCTGGTGTCTCACTGGAATGTCTTCAATTTTCTTATCTCCTA	2275
Qy	2161	AACACTGCAGCTCAGGTTGCTATGCTTCAAGATTTGGTGTCTTATCTAGTGGGCAAC	2220
Db	2276	AACACTGCAGCTCAGGTTGCTATGCTTCAAGATTTGGTGTCTTATCTAGTGGGCAAC	2335
Qy	2221	AAACAAAGTATGCTAAATGTCATCTGTAATGCGAGGAGGAATGTAAACGAGAACTAGAT	2280
Db	2336	AAACAAAGTATGCTAAATGTCATCTGTAATGCGAGGAGGAATGTAAACGAGAACTAGAT	2395
Qy	2281	CTTAACTGGTACTTAGGAAATTTTATCAGGTTTAACTGTAGCTACCGTTCTTTTGGGCATA	2340
Db	2396	CTTAACTGGTACTTAGGAAATTTTATCAGGTTTAACTGTAGCTACCGTTCTTTTGGGCATA	2455
Qy	2341	GCAAGATCTCTATTTGGTATTTCTAGCTCTTGTAACTCTTCAACAACTTTGCAACAACAA	2400
Db	2456	GCAAGATCTCTATTTGGTATTTCTAGCTCTTGTAACTCTTCAACAACTTTGCAACAACAA	2515
Qy	2401	ATGTTTGAGTCAATTTCTGAAAGCTCCCGTATTTATTTTGTAGATAAATCCAATAGGAAGA	2460
Db	2516	ATGTTTGAGTCAATTTCTGAAAGCTCCCGTATTTATTTTGTAGATAAATCCAATAGGAAGA	2575
Qy	2461	ATTTTAAATCGTTTCTCCAAAGACATTTGGAACACTTGTGATGATTTTGTGCGCTGACGTTT	2520
Db	2576	ATTTTAAATCGTTTCTCCAAAGACATTTGGAACACTTGTGATGATTTTGTGCGCTGACGTTT	2635
Qy	2521	TTAGATTTTCAACAGACATTTGCTACAAAGTGGTGGTGTGGTGTCTCTGTGGCTGTGGCGGTG	2580
Db	2636	TTAGATTTTCAACAGACATTTGCTACAAAGTGGTGGTGTGGTGTCTCTGTGGCTGTGGCGGTG	2695
Qy	2581	ATTCCTTTGGATCGCAATACCCCTTGGTTCCCTTGGAAATCATTTTCATTTTCTTCGGGGA	2640
Db	2696	ATTCCTTTGGATCGCAATACCCCTTGGTTCCCTTGGAAATCATTTTTCATTTTCTTCGGGGA	2755



QY 2641 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGAACTCAAACTCGAGTCCAGTG 2700  
DB |||||||  
QY 2756 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGAACTCAAACTCGAGTCCAGTG 2815  
DB |||||||  
QY 2701 TTTTCCCACTTGTGCATCTCTCTCCAGGGCTCTGGACCATTCCGGGATACAAAGCAGAA 2760  
DB |||||||  
QY 2816 TTTTCCCACTTGTGCATCTCTCTCCAGGGCTCTGGACCATTCCGGGATACAAAGCAGAA 2875  
DB |||||||  
QY 2761 GAGAGGTGTGAGGAACCTGTGTGATGACACACAGGATTTACATTGAGGCTTGTCTTGT 2820  
DB |||||||  
QY 2876 GAGAGGTGTGAGGAACCTGTGTGATGACACACAGGATTTACATTGAGGCTTGTCTTGT 2935  
DB |||||||  
QY 2821 TTTTGTGACAACTGTCGGCTGCTGCGTCTGCGATGCACTCTGCGATGCGGGCAGGTTGGT 2880  
DB |||||||  
QY 2936 TTTTGTGACAACTGTCGGCTGCTGCGTCTGCGATGCACTCTGCGATGCGGGCAGGTTGGT 2995  
DB |||||||  
QY 2881 ATCATCGTTGCTTGTGGTCCCTGATCTTGCAAAACCTCTGCGATGCGGGCAGGTTGGT 2940  
DB |||||||  
QY 2996 ATCATCGTTGCTTGTGGTCCCTGATCTTGCAAAACCTCTGCGATGCGGGCAGGTTGGT 3055  
DB |||||||  
QY 2941 TTGCACTGTCTATGCTGCTCACGCTCATGCGGATGTTTCACTGCTGTGTTGCAAAAGT 3000  
DB |||||||  
QY 3056 TTGCACTGTCTATGCTGCTCACGCTCATGCGGATGTTTCACTGCTGTGTTGCAAAAGT 3115  
DB |||||||  
QY 3001 GCTGAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3060  
DB |||||||  
QY 3116 GCTGAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3175  
DB |||||||  
QY 3061 AAAGAAGCACCCTTGGGAATATCAGAAACCGCCACCACGAGCTTGCCCTCATGAAGAGTG 3120  
DB |||||||  
QY 3176 AAAGAAGCACCCTTGGGAATATCAGAAACCGCCACCACGAGCTTGCCCTCATGAAGAGTG 3235  
DB |||||||  
QY 3121 ATAATCTTTGACATGTGAACCTCATGTACAGTCCAGTGGGCTCTGTTACTGAAGCAT 3180  
DB |||||||  
QY 3236 ATAATCTTTGACATGTGAACCTCATGTACAGTCCAGTGGGCTCTGTTACTGAAGCAT 3295  
DB |||||||  
QY 3181 CTGACAGCACTCATTAATCACAAGAAAGGTTGCGCATTTGGGAAGAACCGGAGCTGGA 3240  
DB |||||||  
QY 3296 CTGACAGCACTCATTAATCACAAGAAAGGTTGCGCATTTGGGAAGAACCGGAGCTGGA 3355  
DB |||||||  
QY 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTGAGAACCCGAGGTAAATTTGGATT 3300  
DB |||||||  
QY 3356 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTGAGAACCCGAGGTAAATTTGGATT 3415  
DB |||||||  
QY 3301 GATTAAGATCTTTGACAACTGAAATTTGGAATTCACGATTTAAGGAAGAAATGTCAATCAT 3360  
DB |||||||  
QY 3416 GATTAAGATCTTTGACAACTGAAATTTGGAATTCACGATTTAAGGAAGAAATGTCAATCAT 3475  
DB |||||||  
QY 3361 CCTCAGGAACCTGTTTGTTCACCTGGAAACATGAGGAACCCCTGGATCCCTTTAATGAG 3420  
DB |||||||  
QY 3476 CCTCAGGAACCTGTTTGTTCACCTGGAAACATGAGGAACCCCTGGATCCCTTTAATGAG 3535  
DB |||||||  
QY 3421 CACACGGATGAGGAACCTGTTGAAATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3480  
DB |||||||  
QY 3536 CACACGGATGAGGAACCTGTTGAAATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3595  
DB |||||||  
QY 3481 GATCTTCTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540  
DB |||||||  
QY 3596 GATCTTCTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3655  
DB |||||||  
QY 3541 CAAAGACAACTGTTGCTGCTGCGGCAATCTCAGGAACCAATCAGATATGATGATGATGAT 3600  
DB |||||||  
QY 3656 CAAAGACAACTGTTGCTGCTGCGGCAATCTCAGGAACCAATCAGATATGATGATGATGAT 3715  
DB |||||||  
QY 3601 GATTAAGCGAGGCAATGTTGGATCCAGAACTGATGATGATGATGATGATGATGATGATGAT 3660  
DB |||||||  
QY 3716 GATTAAGCGAGGCAATGTTGGATCCAGAACTGATGATGATGATGATGATGATGATGATGAT 3775  
DB |||||||  
QY 3661 GAGAAATTTGCCCACTGACCGCTGCTAACCAATTGACACACAGATTTGACACCAATTTGAC 3720  
DB |||||||  
QY 3776 GAGAAATTTGCCCACTGACCGCTGCTAACCAATTGACACACAGATTTGACACCAATTTGAC 3835  
DB |||||||  
QY 3721 AGCGACAAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGCTATGTT 3780

DB 3836 AGCGACAAGATATGTTTGTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGATGTT 3895  
QY 3781 TTGCTGCAAAATAAAGAGAGCCTATTTTTCAAGATGTGTGCAACAACCTGGGCAAGGCAGAA 3840  
DB 3896 TTGCTGCAAAATAAAGAGAGCCTATTTTTCAAGATGTGTGCAACAACCTGGGCAAGGCAGAA 3955  
QY 3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATCTTCAAAAGAAATTTATCCACATATT 3900  
DB 3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATCTTCAAAAGAAATTTATCCACATATT 4015  
QY 3901 GGTCACACTGACCACTGTTTACAAACACCTTCCAAATGACAGCCCTCGACCTTAACTATT 3960  
DB 4016 GGTCACACTGACCACTGTTTACAAACACCTTCCAAATGACAGCCCTCGACCTTAACTATT 4075  
QY 3961 TTCGAGACAGCACTGTGA 3978  
DB 4076 TTCGAGACAGCACTGTGA 4093

RESULT 4  
ADH10612  
ID ADH10612 standard; DNA; 5284 BP.  
XX  
AC ADH10612;  
XX  
XX 11-MAR-2004 (first entry)  
DT  
XX Human cancer-related polynucleotide, SEQ ID 2.  
DE  
XX Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
KW  
XX Homo sapiens.  
OS  
XX WO2003104404-A2.  
PN  
XX 18-DEC-2003.  
PD  
XX 05-JUN-2003; 2003WO-US017772.  
PF  
XX 06-JUN-2002; 2002US-0386651P.  
PR  
XX (AVAL-) AVALON PHARM INC.  
PA  
XX Ebner R;  
PI  
XX WPI; 2004-062332/06.  
DR  
XX  
XX Identifying agents that modulate the activity of cancer-related gene,  
PT useful for treating or diagnosing prostate cancer comprising contacting a  
PT compound with a cell containing a gene under conditions promoting  
PT expression of the gene.  
XX  
XX Claim 1; SEQ ID NO 2; 79pp; English.  
PS  
XX  
XX The invention relates to identifying an agent that modulates the activity  
CC of a cancer-related gene. The method involves contacting a compound with  
CC a cell containing a gene that corresponds to a polynucleotide having a  
CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
CC expression of the gene. The method is useful for identifying an agent  
CC that modulates the activity of a cancer-related gene. The polypeptides  
CC and antibodies of the invention are useful for treating and diagnosing  
CC cancer, preferably prostate cancer. It is also useful for screening  
CC assays for agents that are effective in reducing the activity of cancer-  
CC related genes. The present sequence represents a specific example of a  
CC cancer-related polynucleotide sequence.  
XX  
SQ Sequence 5284 BP; 1480 A; 1138 C; 1210 G; 1456 T; 0 U; 0 Other;

Query Match 99.9%; Score 3974.8; DB 12; Length 5284;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



QY 1 ATGCTGCCCGTGTACAGAGGTGAAGCCCAACCCGCTGCAGGAGCGGAACTCTGCTCA 60  
 Db 116 ATGCTGCCCGTGTACAGAGGTGAAGCCCAACCCGCTGCAGGAGCGGAACTCTGCTCA 175  
 QY 61 CGCGTGTCTCTGCTGCTCAATCCCTGTTTAAATTTGGCCATAAAGCGAGATTAGAG 120  
 Db 176 CGCGTGTCTCTGCTGCTCAATCCCTGTTTAAATTTGGCCATAAAGCGAGATTAGAG 235  
 QY 121 GAAGATGATATGATATTCAGTGTCTGCAGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 180  
 Db 236 GAAGATGATATGATATTCAGTGTCTGCAGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 295  
 QY 181 CAAGGTTCTGGATAAAGAGTTTAAAGCTGGAATGAGATGAGCAGAACGCTTCTTTTA 240  
 Db 296 CAAGGTTCTGGATAAAGAGTTTAAAGCTGGAATGAGATGAGCAGAACGCTTCTTTTA 355  
 QY 241 ACAAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
 Db 356 ACAAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 415  
 QY 301 ATTGAGGAAGTGCACCAAGTAAATCCAGCCCATATTTTGGGAAATTTTAAATTTATTTT 360  
 Db 416 ATTGAGGAAGTGCACCAAGTAAATCCAGCCCATATTTTGGGAAATTTTAAATTTATTTT 475  
 QY 361 GAAAATATGATCCCATGGATTCGTGTGCTTTGAACACAGCGTACGCTATGCCACGGTG 420  
 Db 476 GAAAATATGATCCCATGGATTCGTGTGCTTTGAACACAGCGTACGCTATGCCACGGTG 535  
 QY 421 CTGACTTTTGCAGCTCATTTTGGCTATCTGCTATCTGATCACTTATTTTATCAAGTTTCA 480  
 Db 536 CTGACTTTTGCAGCTCATTTTGGCTATCTGCTATCTGATCACTTATTTTATCAAGTTTCA 595  
 QY 481 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 540  
 Db 596 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 655  
 QY 541 CTTAGTAAATGCGCATGGGGAAGAACACACAGGCCAGATGATCAATCTGCTGTCCAAT 600  
 Db 656 CTTAGTAAATGCGCATGGGGAAGAACACACAGGCCAGATGATCAATCTGCTGTCCAAT 715  
 QY 601 GATGTGAACAGTTTGTATCAGTGCACAGTGTCTTACACTTCTGTTGGGAGGACCACTG 660  
 Db 716 GATGTGAACAGTTTGTATCAGTGCACAGTGTCTTACACTTCTGTTGGGAGGACCACTG 775  
 QY 661 CAGCGGATCGCAGTGAATGCTTCTGAGTAGGATAGGAAATATCGTGTCTTGTCTGGG 720  
 Db 776 CAGCGGATCGCAGTGAATGCTTCTGAGTAGGATAGGAAATATCGTGTCTTGTCTGGG 835  
 QY 721 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAAGTTGTTCTCATCA 780  
 Db 836 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAAGTTGTTCTCATCA 895  
 QY 781 CTGAGGAGTAAACCTGCACTTTCAGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840  
 Db 896 CTGAGGAGTAAACCTGCACTTTCAGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955  
 QY 841 ACTGATATAGGATAAATAAATGTAGCCCTGGGAAAGTCAATTTTCAAATCTTATTTACC 900  
 Db 956 ACTGATATAGGATAAATAAATGTAGCCCTGGGAAAGTCAATTTTCAAATCTTATTTACC 1015  
 QY 901 AATTGAGAAAGAGGAGATTTCAAAGATTTCTGAGAAAGTTCTTCTGAGGAGTGAAT 960  
 Db 1016 AATTGAGAAAGAGGAGATTTCAAAGATTTCTGAGAAAGTTCTTCTGAGGAGTGAAT 1075  
 QY 961 TTGCTTCTGTTTTCAGTGCAGCAAAATCATCTGTTTGTGACCTTCAACCATCTAGCTG 1020  
 Db 1076 TTGCTTCTGTTTTCAGTGCAGCAAAATCATCTGTTTGTGACCTTCAACCATCTAGCTG 1135  
 QY 1021 CTCCTCGGAGTGTGATCACAGCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080  
 Db 1136 CTCCTCGGAGTGTGATCACAGCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195  
 QY 1081 GTGGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1140

Db 1196 GTGGGCTGACGGTTACCCCTTCTTCCCTCAGCCATTGAGAGGGTGTTCAGAGCAATC 1255  
 QY 1141 GTACAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGATGAGATATCACAGCGCAACCGT 1200  
 Db 1256 GTACAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGATGAGATATCACAGCGCAACCGT 1315  
 QY 1201 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGCAAGGATTTTACTGCTTTTGGGAT 1260  
 Db 1316 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGCAAGGATTTTACTGCTTTTGGGAT 1375  
 QY 1261 AAGCATCAGAGACCCCACTCTACAGGCCCTTCTTACTGTACAGACCTTGGCGAATTG 1320  
 Db 1376 AAGCATCAGAGACCCCACTCTACAGGCCCTTCTTACTGTACAGACCTTGGCGAATTG 1435  
 QY 1321 TTAGCTGTGGTGGCGCCCGTGGGAGCAGGGAAGTCACTACCTGTTAAAGTCCGCTCGG 1380  
 Db 1436 TTAGCTGTGGTGGCGCCCGTGGGAGCAGGGAAGTCACTACCTGTTAAAGTCCGCTCGG 1495  
 QY 1381 GAATTGGCCCCAAGTCAAGGCTGTGTGAGCGTGCATGGAAGATTTGCCCTATGTCTCAG 1440  
 Db 1496 GAATTGGCCCCAAGTCAAGGCTGTGTGAGCGTGCATGGAAGATTTGCCCTATGTCTCAG 1555  
 QY 1441 CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATTTTATTTGGGAAAGATATCAAA 1500  
 Db 1556 CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATTTTATTTGGGAAAGATATCAAA 1615  
 QY 1501 AAGGAACGATATGAAAGTCAAAAGCTTGTCTCTGAAAAGGATTTACAGCTGTG 1560  
 Db 1616 AAGGAACGATATGAAAGTCAAAAGCTTGTCTCTGAAAAGGATTTACAGCTGTG 1675  
 QY 1561 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGAGGAG 1620  
 Db 1676 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGAGGAG 1735  
 QY 1621 GCAGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCAGAT 1680  
 Db 1736 GCAGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCAGAT 1795  
 QY 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA 1740  
 Db 1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA 1855  
 QY 1741 ATTTTGATCAGAGAGATCAAAATTTTGTGACTCATCAGTTGTCAGTACCTCAAGCTGCA 1800  
 Db 1856 ATTTTGATCAGAGAGATCAAAATTTTGTGACTCATCAGTTGTCAGTACCTCAAGCTGCA 1915  
 QY 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGTGTGCAAGAGGAGCTTACACTGAGTTC 1860  
 Db 1916 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGTGTGCAAGAGGAGCTTACACTGAGTTC 1975  
 QY 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAA 1920  
 Db 1976 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAA 2035  
 QY 1921 CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTTCGTTTGG 1980  
 Db 2036 CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTTCGTTTGG 2095  
 QY 1981 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTGTCTCTGGAGAGCCCAAGATACAGAG 2040  
 Db 2096 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTGTCTCTGGAGAGCCCAAGATACAGAG 2155  
 QY 2041 AATGTCCAGTTACACTATCAGAGGAAACCGTTCTCAAGGAAAGTGGTTTTCAGGCC 2100  
 Db 2156 AATGTCCAGTTACACTATCAGAGGAAACCGTTCTCAAGGAAAGTGGTTTTCAGGCC 2215  
 QY 2101 TATAAGAAATTTACTTTCAGAGCTGGTGTCTCACTGGATTTGTTCTTCTTATTTCTCCTA 2160  
 Db 2216 TATAAGAAATTTACTTTCAGAGCTGGTGTCTCACTGGATTTGTTCTTCTTATTTCTCCTA 2275  
 QY 2161 AACACTGACGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTCATCTCGGCAATC 2220

Db 2276 AACACTGACGCTCAGGTTGGCTATGTGCTTCAAGATTGGTGGCTTTCATATACTGGGCAAC 2335  
Qy 2221 AAACAAAGTATGCTAAATGTCACCTGTAATGGAGGAGGAAATGTAAACCGAAGCTAGAT 2280  
Db 2336 AAACAAAGTATGCTAAATGTCACCTGTAATGGAGGAGGAAATGTAAACCGAAGCTAGAT 2395  
Qy 2281 CTTAACTGGTACTTAAAGAAATTAATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA 2340  
Db 2396 CTTAACTGGTACTTAAAGAAATTAATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA 2455  
Qy 2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTAACTCTTCACAAACTTTGCAACAAAA 2400  
Db 2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTAACTCTTCACAAACTTTGCAACAAAA 2515  
Qy 2401 ATGTTTGAGTCAATCTGAAAGCTCCGGTATTAATCTTTGATAGAAATCCAAATAGGAAGA 2460  
Db 2516 ATGTTTGAGTCAATCTGAAAGCTCCGGTATTAATCTTTGATAGAAATCCAAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635  
Qy 2521 TTAGATTTCATCCAGACATTTGCTACAAAGTGGTTGGTGTGCTCTGTGGCTGTGGCCGTG 2580  
Db 2636 TTAGATTTCATCCAGACATTTGCTACAAAGTGGTTGGTGTGCTCTGTGGCTGTGGCCGTG 2695  
Qy 2581 ATTCTTGGATCGCAATACCTTGGTTCCTTGGTATTCATTTTCTTCGGCGGA 2640  
Db 2696 ATTCTTGGATCGCAATACCTTGGTTCCTTGGTATTCATTTTCTTCGGCGGA 2755  
Qy 2641 TATTTTGGAAACGTCGAAGATGTCGAAGCGCTGGAATCTCAACTCCGAGTCCAGTG 2700  
Db 2756 TATTTTGGAAACGTCGAAGATGTCGAAGCGCTGGAATCTCAACTCCGAGTCCAGTG 2815  
Qy 2701 TTTTCCCACTTGTCACTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760  
Db 2816 TTTTCCCACTTGTCACTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875  
Qy 2761 GAGAGGTGTCAGGAATCTGTTGATGCAACAGATTTACATTCAGAGGCTTGGTCTTG 2820  
Db 2876 GAGAGGTGTCAGGAATCTGTTGATGCAACAGAGATTTACATTCAGAGGCTTGGTCTTG 2935  
Qy 2821 TTTTGGACAACTCCGCTGGTTCGGCTCGTCTGGATGCCATCTGTGCCATGTTTGTG 2880  
Db 2936 TTTTGGACAACTCCGCTGGTTCGGCTCGTCTGGATGCCATCTGTGCCATGTTTGTG 2995  
Qy 2881 ATCATCGTTGGCTTGGCTCCCTGATTTCTGGCAAAAACTCTGATGCGGGCAGGTTGGT 2940  
Db 2996 ATCATCGTTGGCTTGGCTCCCTGATTTCTGGCAAAAACTCTGATGCGGGCAGGTTGGT 3055  
Qy 2941 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTGCAAAAGT 3000  
Db 3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTGCAAAAGT 3115  
Qy 3001 GCTCAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTTGAA 3060  
Db 3116 GCTCAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTTGAA 3175  
Qy 3061 AAAGAAGCACCTTGGGAATATCAGAAACGCCACCAACAGGCTTGGCCCCCATGAAGAGTG 3120  
Db 3176 AAAGAAGCACCTTGGGAATATCAGAAAGCCCAACAGGCTTGGCCCCCATGAAGAGTG 3235  
Qy 3121 ATAACTTTGACAAATGTGAACCTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGCAT 3180  
Db 3236 ATAACTTTGACAAATGTGAACCTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGCAT 3295  
Qy 3181 CTGACAGCACTCATTAATACAAAGAAAGGTGCGCATTTGGGAAGAAACCGGAGCTGGA 3240  
Db 3296 CTGACAGCACTCATTAATACAAAGAAAGGTGCGCATTTGGGAAGAAACCGGAGCTGGA 3355  
Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTGACAAACCGGAGGTAAATTTGGATT 3300  
Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTGACAAACCGGAGGTAAATTTGGATT 3415

Qy 3301 GATAAGATCTTGACAACTGAAATTTGGACTTTCAGATTTTAAGGAGAAAAATGTCAATCATA 3360  
Db 3416 GATAAGATCTTGACAACTGAAATTTGGACTTTCAGATTTTAAGGAGAAAAATGTCAATCATA 3475  
Qy 3361 CCTCAGGAACCTGTTTTGTTTTCACCTGGAAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3420  
Db 3476 CCTCAGGAACCTGTTTTGTTTTCACCTGGAAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3535  
Qy 3421 CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACCTTAAGAAAAACCATTTGAA 3480  
Db 3536 CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACCTTAAGAAAAACCATTTGAA 3595  
Qy 3481 GATCTTCTCGTAAATGATACCTGATTTAGCAGAATCAGATCCCAATTTTAGTGTGGA 3540  
Db 3596 GATCTTCTCGTAAATGATACCTGATTTAGCAGAATCAGATCCCAATTTTAGTGTGGA 3655  
Qy 3541 CAAAGACAACTGGTGTGCTTGGCAGGGCAATCTCAGGAAAAATCAGATATTGATTATT 3600  
Db 3656 CAAAGACAACTGGTGTGCTTGGCAGGGCAATCTCAGGAAAAATCAGATATTGATTATT 3715  
Qy 3601 GATGAACGACGGCAAAATGTGGATCCAAAGAACTGATGAGTTTAATACAAAAAATAATCCGG 3660  
Db 3716 GATGAACGACGGCAAAATGTGGATCCAAAGAACTGATGAGTTTAATACAAAAAATAATCCGG 3775  
Qy 3661 GAGAAATTTGCCCACTGCACCGTCTAACCATTTGCCACACAGATTTGAACCATTTATTGAC 3720  
Db 3776 GAGAAATTTGCCCACTGCACCGTCTAACCATTTGCCACACAGATTTGAACCATTTATTGAC 3835  
Qy 3721 AGGCACAAGATAATGTTTTAGATTTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3780  
Db 3836 AGGCACAAGATAATGTTTTAGATTTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895  
Qy 3781 TTGCTGCAAAATAAAGAGAGCCTATTTTTACAAGATGTGCAACAACTGGGCAAGCGAGAA 3840  
Db 3896 TTGCTGCAAAATAAAGAGAGCCTATTTTTACAAGATGTGCAACAACTGGGCAAGCGAGAA 3955  
Qy 3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACITTCAAAAAGAAATTTATCCACATATT 3900  
Db 3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACITTCAAAAAGAAATTTATCCACATATT 4015  
Qy 3901 GGTCACTGACCACTGTTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACCTATT 3960  
Db 4016 GGTCACTGACCACTGTTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACCTATT 4075  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 4076 TTCGAGACAGCACTGTGA 4093

## RESULT 5

ADH10624  
ID ADH10624 standard; DNA; 5833 BP.  
XX  
AC ADH10624;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human cancer-related polynucleotide, SEQ ID 14.  
XX  
KW Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO2003104404-A2.  
XX  
PD 18-DEC-2003.  
XX  
PF 05-JUN-2003; 2003WO-US017772.  
XX  
PR 06-JUN-2002; 2002US-0386651P.  
XX  
PA (AVAL-) AVALON PHARM INC.

XX Ebner R;  
 XX WPI; 2004-062332/06.  
 XX Identifying agents that modulate the activity of cancer-related gene,  
 PT useful for treating or diagnosing prostate cancer comprising contacting a  
 PT compound with a cell containing a gene under conditions promoting  
 PT expression of the gene.  
 XX  
 PS Claim 1; SEQ ID NO 14; 79pp; English.  
 XX  
 CC The invention relates to identifying an agent that modulates the activity  
 CC of a cancer-related gene. The method involves contacting a compound with  
 CC a cell containing a gene that corresponds to a polynucleotide having a  
 CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
 CC expression of the gene. The method is useful for identifying an agent  
 CC that modulates the activity of a cancer-related gene. The polypeptides  
 CC and antibodies of the invention are useful for treating and diagnosing  
 CC cancer, preferably prostate cancer. It is also useful for screening  
 CC assays for agents that are effective in reducing the activity of cancer-  
 CC related genes. The present sequence represents a specific example of a  
 CC cancer-related polynucleotide sequence.  
 XX  
 SQ Sequence 5833 BP; 1660 A; 1175 C; 1306 G; 1692 T; 0 U; 0 Other;

Query Match 99.9%; Score 3974.8; DB 12; Length 5833;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCTGCCGTGTACAGAGGTGAAGCCCAACCGCTGCAGGACGCGAACCTCTGCTCA 60  
 Db 116 ATGCTGCCGTGTACAGAGGTGAAGCCCAACCGCTGCAGGACGCGAACCTCTGCTCA 175

Qy 61 CGCGTGTCTCTGGTGGTCAATCCCTGTTTAAATTTGATGAGGAGGAGTAGAG 120  
 Db 176 CGCGTGTCTCTGGTGGTCAATCCCTGTTTAAATTTGATGAGGAGGAGTAGAG 235

Qy 121 GAAGATGATATGATTCAGTCTGCTGCAAGACCGCTCACAGACCTTTGGAGAGGATTG 180  
 Db 236 GAAGATGATATGATTCAGTCTGCTGCAAGACCGCTCACAGACCTTTGGAGAGGATTG 295

Qy 181 CAAGGGTTCGGGATAAAGAGTTTAAAGAGCTGAGAAATGCGACAGAACCTTCTTTA 240  
 Db 296 CAAGGGTTCGGGATAAAGAGTTTAAAGAGCTGAGAAATGCGACAGAACCTTCTTTA 355

Qy 241 ACAGAGCAATCATAAAGTGTACTGGAATCTTATTAGTTTGGGAATTTTACGTTA 300  
 Db 356 ACAGAGCAATCATAAAGTGTACTGGAATCTTATTAGTTTGGGAATTTTACGTTA 415

Qy 301 ATTGAGGAAGTGCAGAAATGATCCAGCCCATATTTTGGGAAAAATTTATTATTTT 360  
 Db 416 ATTGAGGAAGTGCAGAAATGATCCAGCCCATATTTTGGGAAAAATTTATTATTTT 475

Qy 361 GAAATATTATGATCCCATGATTTCTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 420  
 Db 476 GAAATATTATGATCCCATGATTTCTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 535

Qy 421 CTGACTTTTTCAGCTCATTTTGGCTATACATGATCATATTTATTTTATCAGTTTCAG 480  
 Db 536 CTGACTTTTTCAGCTCATTTTGGCTATACATGATCATATTTATTTTATCAGTTTCAG 595

Qy 481 TGTCTGGGATGAGTTACGATGAGCATGCGCATATTTTATCGGAAGGCACTTCGT 540  
 Db 596 TGTCTGGGATGAGTTACGATGAGCATGCGCATATTTTATCGGAAGGCACTTCGT 655

Qy 541 CTTAGTAACATGGCCATGGGGAAGCAACCAACAGCCAGATAGTCAATCTCTGCTCCAAT 600  
 Db 656 CTTAGTAACATGGCCATGGGGAAGCAACCAACAGCCAGATAGTCAATCTCTGCTCCAAT 715

Qy 601 GATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG 660  
 Db 716 GATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG 775

Qy 661 CAGCGATCGCAGTGAATGCGCTTACTCTGGATGGAGTAGGAATATCGTGCCTTCTCTGGG 720  
 Db 776 CAGCGATCGCAGTGAATGCGCTTACTCTGGATGGAGTAGGAATATCGTGCCTTCTCTGGG 835

Qy 721 ATGGAGTCTTAATCAATCTCTGCCCTTGAAGAGTGTGTTGGGAAGTGTCTTCATCA 780  
 Db 836 ATGGAGTCTTAATCAATCTCTGCCCTTGAAGAGTGTGTTGGGAAGTGTCTTCATCA 895

Qy 781 CTGAGGAGTAAACCTGCAACCTTTCCAGGATGCCAGGATCAGACCATCAATGAAGTTATA 840  
 Db 896 CTGAGGAGTAAACCTGCAACCTTTCCAGGATGCCAGGATCAGACCATCAATGAAGTTATA 955

Qy 841 ACTGGTATAAGGATAATAAATGTAGCCCTGGGAAAAGTCAATTTCAAATCTTATTACC 900  
 Db 956 ACTGGTATAAGGATAATAAATGTAGCCCTGGGAAAAGTCAATTTCAAATCTTATTACC 1015

Qy 901 AATTGAGAAAGAGGAGATTTCAGAGATTCCTGAGAGTTCCTGCTCAGGGGGATGAAT 960  
 Db 1016 AATTGAGAAAGAGGAGATTTCAGAGATTCCTGAGAGTTCCTGCTCAGGGGGATGAAT 1075

Qy 961 TTGGCTTCGTTTTCAGTGCAGCAAGCAAAATCATCGTGTGTTGACCTTCACCACTACCGT 1020  
 Db 1076 TTGGCTTCGTTTTCAGTGCAGCAAGCAAAATCATCGTGTGTTGACCTTCACCACTACCGT 1135

Qy 1021 CTCCTCGCAGTGTGATCACAGCCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080  
 Db 1136 CTCCTCGCAGTGTGATCACAGCCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy 1081 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGCAATC 1140  
 Db 1196 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGCAATC 1255

Qy 1141 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTGATGAGATATCACAGCGCAACCGT 1200  
 Db 1256 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTGATGAGATATCACAGCGCAACCGT 1315

Qy 1201 CAGCTGCGCTCAGATGTTAAAGATGTTGATGTCAGGAGTATTTACTGCTTTTGGGAT 1260  
 Db 1316 CAGCTGCGCTCAGATGTTAAAGATGTTGATGTCAGGAGTATTTACTGCTTTTGGGAT 1375

Qy 1261 AAGCATCAGAGACCCCAACTCTAACAGGCTTTCTTTACTGTCAGACCTGGGGAATTG 1320  
 Db 1376 AAGCATCAGAGACCCCAACTCTAACAGGCTTTCTTTACTGTCAGACCTGGGGAATTG 1435

Qy 1321 TTAGCTGTGCTCGGCGCGCTGGGAGCAGGAGTATCATCTGTTAAGTGCCTGCTCGGG 1380  
 Db 1436 TTAGCTGTGCTCGGCGCGCTGGGAGCAGGAGTATCATCTGTTAAGTGCCTGCTCGGG 1495

Qy 1381 GAATTGGCCCCAAGTCAAGCGCTGCTCAGCGTGCATGGAAGAAATGCTATGCTCTCAG 1440  
 Db 1496 GAATTGGCCCCAAGTCAAGCGCTGCTCAGCGTGCATGGAAGAAATGCTATGCTCTCAG 1555

Qy 1441 CAGCCCTGGGTGTTCTCGGGAATCTCTCAGGAGTAAATTTTATTTGGGAAGAAATACGAA 1500  
 Db 1556 CAGCCCTGGGTGTTCTCGGGAATCTCTCAGGAGTAAATTTTATTTGGGAAGAAATACGAA 1615

Qy 1501 AAGGAACGATATGAAAGAGTCAAAAGCTTGTGCTCTGAAAAGGATTTTACAGCTGTTG 1560  
 Db 1616 AAGGAACGATATGAAAGAGTCAAAAGCTTGTGCTCTGAAAAGGATTTTACAGCTGTTG 1675

Qy 1561 GAGGATGCTGATCTGATGATAGGAGATCGGGGAACCGCTGAGTGGAGGGCAGAAA 1620  
 Db 1676 GAGGATGCTGATCTGATGATAGGAGATCGGGGAACCGCTGAGTGGAGGGCAGAAA 1735

Qy 1621 GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATCTGACATCTATCTCTCGGACGAT 1680  
 Db 1736 GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATCTGACATCTATCTCTCGGACGAT 1795

Qy 1681 CCTCTCAGTGCAGTATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAA 1740  
 Db 1796 CCTCTCAGTGCAGTATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAA 1855

QY 1741 ATTTTGCATGAGAAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCABAAGCTGCA 1800  
DB 1856 ATTTTGCATGAGAAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCABAAGCTGCA 1915  
QY 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAATAATGCTGCAGAAGGGGACTTACACTGAGTTC 1860  
DB 1916 AGTCAGATTTCTGATATTTGAAAGATGGTAATAATGCTGCAGAAGGGGACTTACACTGAGTTC 1975  
QY 1861 CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGAAACAA 1920  
DB 1976 CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGAAACAA 2035  
QY 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGCGTTTGG 1980  
DB 2036 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGCGTTTGG 2095  
QY 1981 TCTCAACAATCTTCTAGACCCCTCCTTGAAGAATGGTCTCTGGAGAGCCAAAGATACAGAG 2040  
DB 2096 TCTCAACAATCTTCTAGACCCCTCCTTGAAGAATGGTCTCTGGAGAGCCAAAGATACAGAG 2155  
QY 2041 AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2100  
DB 2156 AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2215  
QY 2101 TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGAATGTTCTTCATTTTCCTTATTTCTCCTA 2160  
DB 2216 TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGAATGTTCTTCATTTTCCTTATTTCTCCTA 2275  
QY 2161 AACACTGCAGCTCAGGTTGCTCTATGTGCTTCAAGATTTGGTGGCTTTCATCTCGGGCAAAC 2220  
DB 2276 AACACTGCAGCTCAGGTTGCTCTATGTGCTTCAAGATTTGGTGGCTTTCATCTCGGGCAAAC 2335  
QY 2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAATGTAAACGAGAAGCTAGAT 2280  
DB 2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAATGTAAACGAGAAGCTAGAT 2395  
QY 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTTCCTTTTGGGCATA 2340  
DB 2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTTCCTTTTGGGCATA 2455  
QY 2341 GCAAGATCTCTATTTGGTATTTCTACGTCTCTGTTAACTCTTCACAAAACCTTTGCAACAA 2400  
DB 2456 GCAAGATCTCTATTTGGTATTTCTACGTCTCTGTTAACTCTTCACAAAACCTTTGCAACAA 2515  
QY 2401 ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATCTTTGTAGTAGAATPCCAATAGGAAGA 2460  
DB 2516 ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATTTCTTTGATAGAAATPCCAATAGGAAGA 2575  
QY 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACCGTTT 2520  
DB 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACCGTTT 2635  
QY 2521 TTAGATTTTCATCCAGACATTTCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCCGTG 2580  
DB 2636 TTAGATTTTCATCCAGACATTTCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCCGTG 2695  
QY 2581 ATTCTTTGATGCAATACCTTGGTTCCTTGGTATTCATTTTTCATTTTCTTCGCGGA 2640  
DB 2696 ATTCTTTGATGCAATACCTTGGTTCCTTGGTATTCATTTTTCATTTTCTTCGCGGA 2755  
QY 2641 TATTTTGGAAACGTCNAGAGATGTGNAAGCCCTGGGAATCTACAATCCGAGTCCAGTG 2700  
DB 2756 TATTTTGGAAACGTCNAGAGATGTGNAAGCCCTGGGAATCTACAATCCGAGTCCAGTG 2815  
QY 2701 TTTTCCCACTTGTCACTCTTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAAGCAGAA 2760  
DB 2816 TTTTCCCACTTGTCACTCTTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAAGCAGAA 2875  
QY 2761 GAGAGGTGTCAAGAACTGTTTGTATGCAACACAGGATTTACATTCAGAGGCTTGTGTTCTTG 2820  
DB 2876 GAGAGGTGTCAAGAACTGTTTGTATGCAACACAGGATTTACATTCAGAGGCTTGTGTTCTTG 2935  
QY 2821 TTTTGTGACAAAGCTCCCGCTGGTTCCGCGTCCGTCGATGCCATCTGTGCCATGTTTGTGTC 2880

DB 2936 TTTTGTGACAGGTCGCCCTGGTTCCGCTCGTCTGATGCCATCTGTGCCATGTTTGTGTC 2995  
QY 2881 ATCATCGTTCCCTTTGGGTCCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 2940  
DB 2996 ATCATCGTTCCCTTTGGGTCCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 3055  
QY 2941 TTGGCACTGTCTATGCTCCCTCAGCTCATCGGGGATGTTTCAGTGGTGTGTTCCGACAAAGT 3000  
DB 3056 TTGGCACTGTCTATGCTCCCTCAGCTCATCGGGGATGTTTCAGTGGTGTGTTCCGACAAAGT 3115  
QY 3001 GCTCAAGTCTCAGAAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTTGAA 3060  
DB 3116 GCTCAAGTCTCAGAAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTTGAA 3175  
QY 3061 AAAGAACACCTTTGGGAATATCAGAAACGCCACCAACAGCTGGCCCCCATGAAAGGAGTG 3120  
DB 3176 AAAGAACACCTTTGGGAATATCAGAAACGCCACCAACAGCTGGCCCCCATGAAAGGAGTG 3235  
QY 3121 ATAATCTTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCCCTCTGGTACTGAAGCAT 3180  
DB 3236 ATAATCTTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCCCTCTGGTACTGAAGCAT 3295  
QY 3181 CTGACAGCACTCTATTAATCAAGAAAGAGTGGCATTTGTGGGAAGAACCGGAGCTGGA 3240  
DB 3296 CTGACAGCACTCTATTAATCAAGAAAGAGTGGCATTTGTGGGAAGAACCGGAGCTGGA 3355  
QY 3241 AAAAGTCCCTCATCTCAGCCCTTTTGTAGATTTGTAGAACCCGAAAGTAAATTTGGAT 3300  
DB 3356 AAAAGTCCCTCATCTCAGCCCTTTTGTAGATTTGTAGAACCCGAAAGTAAATTTGGAT 3415  
QY 3301 GATAAGATCTTGACAACTGAAATTTGACATTTCAAGATTTAAGGAAGAAATGTCAATCATA 3360  
DB 3416 GATAAGATCTTGACAACTGAAATTTGACATTTCAAGATTTAAGGAAGAAATGTCAATCATA 3475  
QY 3361 CCTCAGGAACTGTGTTTGTCTCCTGGAACAATGAGGAAACCTCTGGATCCCTTTAATGAG 3420  
DB 3476 CCTCAGGAACTGTGTTTGTCTCCTGGAACAATGAGGAAACCTCTGGATCCCTTTAATGAG 3535  
QY 3421 CACACGGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCAATTGAA 3480  
DB 3536 CACACGGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCAATTGAA 3595  
QY 3481 GATCTTCTCGTAAATTTGGATCTGGAATTTAGCAGAACTCAGATCCCAATTTTAGTGTGGA 3540  
DB 3596 GATCTTCTCGTAAATTTGGATCTGGAATTTAGCAGAACTCAGATCCCAATTTTAGTGTGGA 3655  
QY 3541 CAAAGACAACTGGTGTGCTTTCAGGGCAATTTCTCAGGAAACCTCAGATATTCAGATTTAT 3600  
DB 3656 CAAAGACAACTGGTGTGCTTTCAGGGCAATTTCTCAGGAAACCTCAGATATTCAGATTTAT 3715  
QY 3601 GATGAACGCAACGCAAAATGTGGAATCCCAAGAACCTGATGAGTTAATAAAAAAATCCGG 3660  
DB 3716 GATGAACGCAACGCAAAATGTGGAATCCCAAGAACCTGATGAGTTAATAAAAAAATCCGG 3775  
QY 3661 GAGAAATTTGCCCACTGCAACCGTCTTAACCAATTTGCAACAGATTTGAACCAATTTAGAC 3720  
DB 3776 GAGAAATTTGCCCACTGCAACCGTCTTAACCAATTTGCAACAGATTTGAACCAATTTAGAC 3835  
QY 3721 AGCGACAAGATTAATGTTTGTAGATTTAGGAAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
DB 3836 AGCGACAAGATTAATGTTTGTAGATTTAGGAAAGACTGAAAGAAATATGATGAGCCGTATGTT 3895  
QY 3781 TTGCTGCAAAATAAAGAGAGCTATTTTACAAGATGTGTCAACCAACTGGGCAAGGAGAA 3840  
DB 3896 TTGCTGCAAAATAAAGAGAGCTATTTTACAAGATGTGTCAACCAACTGGGCAAGGAGAA 3955  
QY 3841 GCCCTGCCCTCACTGAAAACGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 3900  
DB 3956 GCCCTGCCCTCACTGAAAACGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4015  
QY 3901 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGGAACAGGCCCTCGACCTTAACTATT 3960

Db 4016 GGTCACTGACCAACATGGTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACCTATT 4075  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 6  
ADH10626  
ID ADH10626 standard; DNA; 5862 BP.  
XX  
AC ADH10626;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human cancer-related polynucleotide, SEQ ID 16.  
XX  
KW Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003104404-A2.  
XX  
PD 18-DEC-2003.  
XX  
PF 05-JUN-2003; 2003WO-US017772.  
XX  
PR 06-JUN-2002; 2002US-0386651P.  
XX  
PA (AVAL-) AVALON PHARM INC.  
XX  
PI Ebner R;  
XX  
DR WPI; 2004-062332/06.  
XX

Identifying agents that modulate the activity of cancer-related gene,  
PT useful for treating or diagnosing prostate cancer comprising contacting a  
PT compound with a cell containing a gene under conditions promoting  
PT expression of the gene.  
XX  
PS Claim 1; SEQ ID NO 16; 79pp; English.  
XX

The invention relates to identifying an agent that modulates the activity  
CC of a cancer-related gene. The method involves contacting a compound with  
CC a cell containing a gene that corresponds to a polynucleotide having a  
CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
CC expression of the gene. The method is useful for identifying an agent  
CC that modulates the activity of a cancer-related gene. The polypeptides  
CC and antibodies of the invention are useful for treating and diagnosing  
CC cancer, preferably prostate cancer. It is also useful for screening  
CC assays for agents that are effective in reducing the activity of cancer-  
CC related genes. The present sequence represents a specific example of a  
CC cancer-related polynucleotide sequence.  
XX

Sequence 5862 BP; 1645 A; 1208 C; 1328 G; 1681 T; 0 U; 0 Other;  
SQ

Query Match 99.9%; Score 3974.8; DB 12; Length 5862;  
Best Local Similarity 99.9%; Pred No. 0;  
Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCTGCCCGGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60  
Db 116 ATGCTGCCCGGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 175

Qy 61 CGCGTGTCTTCGTGGTGGCTCAATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAG 120  
Db 176 CGCGTGTCTTCGTGGTGGCTCAATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAG 235

Qy 121 GAAGATGATATGATTTCAGTGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180  
Db 236 GAAGATGATATGATTTCAGTGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 295

Qy 181 CAAGGGTTCTGGGATAAAGAAGTTTTTAAGAGCTGAGAATGACGCA CAGAAGCCTTCTTTA 240

Db 296 CAAGGGTTCTGGGATAAAGAAGTTTTTAAGAGCTGAGAATGACGCA CAGAAGCCTTCTTTA 355  
Qy 241 ACAAGAGCAATATCAAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTA 300  
Db 356 ACAAGAGCAATATCAAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTA 415  
Qy 301 ATTGAGGAAAGTGCACCAAGTAATCCAGCCCATATTTTGGGAAAAATTTATTAATTTT 360  
Db 416 ATTGAGGAAAGTGCACCAAGTAATCCAGCCCATATTTTGGGAAAAATTTATTAATTTT 475  
Qy 361 GAAAAATTATGATCCCATGGATTCTGTGGCTTTTGAACACAGCGTACGCCATATGCCACG 420  
Db 476 GAAAAATTATGATCCCATGGATTCTGTGGCTTTTGAACACAGCGTACGCCATATGCCACG 535  
Qy 421 CTGACTTTTTCGACGCTCAATTTTGGCTTACTGCTATCTGCTATCTATTTTATCAGTTTCAG 480  
Db 536 CTGACTTTTTCGACGCTCAATTTTGGCTTACTGCTATCTGCTATCTATTTTATCAGTTTCAG 595  
Qy 481 TGTGCTGGGATGAGGTTACGAGTAGCCATATGTCCTATATGATTATCGGAAGCACTTCGT 540  
Db 596 TGTGCTGGGATGAGGTTACGAGTAGCCATATGTCCTATATGATTATCGGAAGCACTTCGT 655  
Qy 541 CTTAGTAACATGCGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGTCCTCAAT 600  
Db 656 CTTAGTAACATGCGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGTCCTCAAT 715  
Qy 601 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGTCGGCAGGACCACTG 660  
Db 716 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGTCGGCAGGACCACTG 775  
Qy 661 CAGGCGATCGCAGTACTGCTACTCTGATGAGATAGGAATATCGTGCCTTGTCTGGG 720  
Db 776 CAGGCGATCGCAGTACTGCTACTCTGATGAGATAGGAATATCGTGCCTTGTCTGGG 835  
Qy 721 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAAAGCTGTTTGGAAAGTTGTTCTCATCA 780  
Db 836 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAAAGCTGTTTGGAAAGTTGTTCTCATCA 895  
Qy 781 CTGAGGATTAACACTGCAACTTTTACCGATGCCAGGATCAGGACCATGATGAATTTA 840  
Db 896 CTGAGGATTAACACTGCAACTTTTACCGATGCCAGGATCAGGACCATGATGAATTTA 955  
Qy 841 ACTGTTATAAGGATAATAAAATGTACGCTGGGAAAAGTCATTTCAAATCTTATTAACC 900  
Db 956 ACTGTTATAAGGATAATAAAATGTACGCTGGGAAAAGTCATTTCAAATCTTATTAACC 1015  
Qy 901 AATTGAGAAAGAGGAGATTTTCAAGATTCTGAGAAAGTTCTCTCCCTCAGGGGATGAAT 960  
Db 1016 AATTGAGAAAGAGGAGATTTTCAAGATTCTGAGAAAGTTCTCTCCCTCAGGGGATGAAT 1075  
Qy 961 TTGGCTTCGTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCACCACTACG 1020  
Db 1076 TTGGCTTCGTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCACCACTACG 1135  
Qy 1021 CTCCTCGGCGAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGATGGGCT 1080  
Db 1136 CTCCTCGGCGAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGATGGGCT 1195  
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Db 1196 GTGCGGCTGACGGTTACCCCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1255  
Qy 1141 GTCAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGTATGATATCACAGCGCAACCGT 1200  
Db 1256 GTCAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGTATGATATCACAGCGCAACCGT 1315  
Qy 1201 CAGCTGCCGTGAGATGGTAAAGATGCTGATGTGAGGATTTTACTGCTTTTGGAT 1260  
Db 1316 CAGCTGCCGTGAGATGGTAAAGATGCTGATGTGAGGATTTTACTGCTTTTGGAT 1375  
Qy 1261 AAGGCATCAGAGACCCCACTCTACAGGCGCTTCTTTTACTGTGACAGCTTGCGCAATTG 1320

Db 1376 AAGCATCAGAGACCCCAACTCTACAGGCCCTTTCCTTTACTGTGACACCTGGCGAATTG 1435  
Qy 1321 TTAGCTGTGTCGCGCCCGTGGAGCAGGGAAGTCATCATCTGTTAAAGTGCCTGCTCGGG 1380  
Db 1436 TTAGCTGTGTCGCGCCCGTGGAGCAGGGAAGTCATCATCTGTTAAAGTGCCTGCTCGGG 1495  
Qy 1381 GAATTGGCCCAAGTCAGCGGCTGGTCAGCGTGCATGGAGAAATTCCTATGTGTCACAG 1440  
Db 1496 GAATTGGCCCCAAGTCAGCGGCTGGTCAGCGTGCATGGAGAAATTCCTATGTGTCACAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGAACTCTCAGAGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
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Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTTGCTCTGAAAAAGGATTTACAGCTGTG 1560  
Db 1616 AAGGAACGATATGAAAAGTCATAAAGCTTTGCTCTGAAAAAGGATTTACAGCTGTG 1675  
Qy 1561 GAGGATGGTGTATCTGATGTATAGGAGATCGGGGACCAACGCTGAGTGGAGGCGAGAA 1620  
Db 1676 GAGGATGGTGTATCTGATGTATAGGAGATCGGGGAAACCAACGCTGAGTGGAGGCGAGAA 1735  
Qy 1621 GCAGGCTAAACCTTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT 1680  
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Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACAATTGTTGCAACTGTGTATTTGTCAA 1740  
Db 1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACAATTGTTGCAACTGTGTATTTGTCAA 1855  
Qy 1741 ATTTTGCATGAGAGATGCAAAATTTTGTAGTGCATCATCAGTTGCACTACCTCAAGCTGCA 1800  
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Qy 1801 AGTCAGATTTCTGATATTGAAAGATGGTAAATGTGTGAGAGGGGCACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATATTGAAAGATGGTAAATGTGTGAGAGGGGCACTTACACTGAGTTC 1975  
Qy 1861 CTAAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAGTGAACAA 1920  
Db 1976 CTAAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
Db 2036 CCTCCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095  
Qy 1981 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGATACAGAG 2040  
Db 2096 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGATACAGAG 2155  
Qy 2041 AATGTCCAGTTCACATATCAGAGAGAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCC 2100  
Db 2156 AATGTCCAGTTCACATATCAGAGAGAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCC 2215  
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Db 2216 TATAAGAAATTTACTTCAGAGCTGGTGTCTCAGTGAATGTCTTCTATTTTCTTATTTCTCCTA 2275  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTTCATCTCGGCGAAAC 2220  
Db 2276 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTTCATCTCGGCGAAAC 2335  
Qy 2221 AACAAAGATATGCTAAATGTCACTGTAAATGGAGAGGAAATGTAAACCGAGAACTAGAT 2280  
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Qy 2281 CTTAACTGGTACTTAGGAATTTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2340  
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Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCCTGTGTTAACTCTTCAAAAATTTTGCACAAACAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTAGCTCCTGTGTTAACTCTTCAAAAATTTTGCACAAACAA 2515

Qy 2401 ATGTTTGAATCAATTTCTGAAAGCTCCGGTATTATTCTTTTATAGAAATCCAATAGGAAGA 2460  
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Qy 2461 ATTTTAAATCGTTTCTCCTAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTCAGCGTTT 2520  
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Qy 2521 TTAGATTTTCAATCAGACATTTGCTACAAAGTGGTGGTGTCTCTGTGGCTGTGCCCGTG 2580  
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Qy 2581 ATTCCTTGGATGCAATACCTTGGTTCCTCTGGAAATCAATTTTCAATTTTCTTCGCGGA 2640  
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Qy 2641 TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGAAATCTACAACTCGGAGTCCAGTG 2700  
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Qy 3001 GCTGAAGTCAGAAATATGATGATCTCAGTAGAAAGGTCATTTGAATACACAGACTTTGAA 3060  
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Qy 3061 AAAGAGCACTTTGGGAATATCAGAAACGCCCAACACAGCCTGGCCCCATGAAAGGAGTG 3120  
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Qy 3121 ATATCTTTGACAAATGAACTTCACTGACAGTCCAGTGGGCTCTGTTACTGAAAGCAT 3180  
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Db 3536 CACACGATGAGGAACCTGTGGATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA 3595







Db 776 CAGCGATCGCAGTGAATCGCCCTACTCTGGATGAGATAGGAATATCGTGCCTTGCTGGG 835  
Qy 721 ATGCGAGTCTAATCATCTCTGCCCTTGCAAGAGCTGTTTGGGAAGTTGTTCTCATCA 780  
Db 836 ATGCGAGTCTAATCATCTCTGCCCTTGCAAGAGCTGTTTGGGAAGTTGTTCTCATCA 895  
Qy 781 CTGAGGAGTAAACCTGCAACTTTTCACGATGCCAGATCAGGACCATGAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAACCTGCAACTTTTCACGATGCCAGATCAGGACCATGAATGAAGTTATA 955  
Qy 841 ACTGGTATAAGGATAATAAAATGTAGCCCTGGGAAAAGTCATTTCAAATCTTATTACC 900  
Db 956 ACTGGTATAAGGATAATAAAATGTAGCCCTGGGAAAAGTCATTTCAAATCTTATTACC 1015  
Qy 901 AATTTGAGAAAGAGAGATTTCAAGATTTGAGAAAGTTCTGCCCTCAGGGGATGAAT 960  
Db 1016 AATTTGAGAAAGAGAGATTTCAAGATTTGAGAAAGTTCTGCCCTCAGGGGATGAAT 1075  
Qy 961 TTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCACCACTACGTG 1020  
Db 1076 TTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCACCACTACGTG 1135  
Qy 1021 CTCCTCGGCAGTGTGATCACAGCAGCGCGTGTTCGTGGCAGTGAACGTGTATGGGGCT 1080  
Db 1136 CTCCTCGGCAGTGTGATCACAGCAGCGCGTGTTCGTGGCAGTGAACGTGTATGGGGCT 1195  
Qy 1081 GTGGGCTGACGGTTACCTCTTCTGCCCTCAGCCATGAGAGGTGTGAGGGAATC 1140  
Db 1196 GTGGGCTGACGGTTACCTCTTCTGCCCTCAGCCATGAGAGGTGTGAGAGGGAATC 1255  
Qy 1141 GTACGATCCGAGAAATCCAGACCTTTTGTGCTACTGTGATGAGATATCACAGCGCAACCGT 1200  
Db 1256 GTACGATCCGAGAAATCCAGACCTTTTGTGCTACTGTGATGAGATATCACAGCGCAACCGT 1315  
Qy 1201 CAGCTGGCGTCAGATGGTAAAGATGGTGCATGTCAGGAGTTTACTGCTTTTTGGGAT 1260  
Db 1316 CAGCTGGCGTCAGATGGTAAAGATGGTGCATGTCAGGAGTTTACTGCTTTTTGGGAT 1375  
Qy 1261 AAGGCATCAGAGACCCCACTCAAGGCCCTTCTTACTGTACAGACCTGGGGAATTG 1320  
Db 1376 AAGGCATCAGAGACCCCACTCAAGGCCCTTCTTACTGTACAGACCTGGGGAATTG 1435  
Qy 1321 TTAGCTGTGGTGGCCCGTGGAGCAGGGAAGTCATCACTGTTAAGTCCGCTCGGG 1380  
Db 1436 TTAGCTGTGGTGGCCCGTGGAGCAGGGAAGTCATCACTGTTAAGTCCGCTCGGG 1495  
Qy 1381 GAATGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAAATGGCTATGTCTCAG 1440  
Db 1496 GAATGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAAATGGCTATGTCTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGGAACCTGAGGAGTAATATTTTATTTGGGAAGAAATAGAA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGGAACCTGAGGAGTAATATTTTATTTGGGAAGAAATAGAA 1615  
Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGAAATACAGCTGTG 1560  
Db 1616 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGAAATACAGCTGTG 1675  
Qy 1561 GAGGATGGTGAATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA 1620  
Db 1676 GAGGATGGTGAATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA 1735  
Qy 1621 GCAGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACGAT 1680  
Db 1736 GCAGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACGAT 1795  
Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACGTGTATTGTCAA 1740  
Db 1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACGTGTATTGTCAA 1855  
Qy 1741 ATTTTGCATGAGAGATCACAAATTTTAGTGACTCATCAGTTGTCAGTACCTCAAGAGCTGCA 1800  
Db 1856 ATTTTGCATGAGAGATCACAAATTTTAGTGACTCATCAGTTGTCAGTACCTCAAGAGCTGCA 1915

Qy 1801 AGTCAGATTTCTGATATTGAAGATGGTAAATTGGTGCAGAGGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATATTGAAGATGGTAAATTGGTGCAGAGGGGACTTACACTGAGTTC 1975  
Qy 1861 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAACAA 1920  
Db 1976 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAATCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCCGGTTGG 1980  
Db 2036 CCTCCAGTTCAGGAATCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCCGGTTGG 2095  
Qy 1981 TCTCAAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGATACAGAG 2040  
Db 2096 TCTCAAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGATACAGAG 2155  
Qy 2041 AATGTCCAGTTCACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTTTCAGGCC 2100  
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Qy 2101 TATAAGAAATTTACTCAGAGCTGGTGTCTCATGGAATGTCATTCTTCTTATTCTCCTA 2160  
Db 2216 TATAAGAAATTTACTCAGAGCTGGTGTCTCATGGAATGTCATTCTTCTTATTCTCCTA 2275  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTCATCTGGGCAAAAC 2220  
Db 2276 AACACTGCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTCATCTGGGCAAAAC 2335  
Qy 2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGAAATGTAAACGAGAACTAGAT 2280  
Db 2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGAAATGTAAACGAGAACTAGAT 2395  
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Db 2396 CTAACTGGTACTTTAGGAATTTTATTCAGGTTTAACTGTAGTACCGTTCCTTTTGGGATA 2455  
Qy 2341 GCAGATCTCTATTTGGTATTTCTAGCTCTTGTAACTCTTCAAAAATTTTGCACAAACAA 2400  
Db 2456 GCAGATCTCTATTTGGTATTTCTAGCTCTTGTAACTCTTCAAAAATTTTGCACAAACAA 2515  
Qy 2401 ATGTTTCAGTCAATTTCTGAAAGCTCCCGTATTTTCTTGTATGAAATCCAATAGGAAGA 2460  
Db 2516 ATGTTTCAGTCAATTTCTGAAAGCTCCCGTATTTTCTTGTATGAAATCCAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACGTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACGTTT 2635  
Qy 2521 TTAGATTTTCATCCAGACATTTGCTACAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2580  
Db 2636 TTAGATTTTCATCCAGACATTTGCTACAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2695  
Qy 2581 ATTCCTTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCAATTTTCTTTCGCGGA 2640  
Db 2696 ATTCCTTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCAATTTTCTTTCGCGGA 2755  
Qy 2641 TATTTTGGAAACGCTCAAGAGATGTGAAGCGCTGGAAATCTACAACTCGGAGTCCAGTG 2700  
Db 2756 TATTTTGGAAACGCTCAAGAGATGTGAAGCGCTGGAAATCTACAACTCGGAGTCCAGTG 2815  
Qy 2701 TTTTTCACATTTGTCATCTCTCCAGGGCTCTGGACCATCCCGGATACAAAGCAGAA 2760  
Db 2816 TTTTTCACATTTGTCATCTCTCCAGGGCTCTGGACCATCCCGGATACAAAGCAGAA 2875  
Qy 2761 GAGAGTGTTCAGGAATCTGTTTGTATGCACACAGGATTTTACATTCAGAGGCTTGTCTTTG 2820  
Db 2876 GAGAGTGTTCAGGAATCTGTTTGTATGCACACAGGATTTTACATTCAGAGGCTTGTCTTTG 2935  
Qy 2821 TTTTGTGACAGCTCCCGCTGGTTCGCGCTCGTCTGATGCCATCTGTGCCATGTTTGTCTC 2880  
Db 2936 TTTTGTGACAGCTCCCGCTGGTTCGCGCTCGTCTGATGCCATCTGTGCCATGTTTGTCTC 2995

2881 ATCATCGTGGCTTGGCTCCCTGATCTCTGCAAAACCTCTGGATGCGGCGAGGTTGGT 2940  
 Db ATCATCGTGGCTTGGCTCCCTGATCTCTGCAAAACCTCTGGATGCGGCGAGGTTGGT 3055  
 2941 TTGGCACTGCTTATGCTCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
 Db TTGGCACTGCTTATGCTCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3115  
 3056 TTGGCACTGCTTATGCTCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3115  
 3001 GCTGAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3060  
 Db GCTGAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3175  
 3116 GCTGAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3175  
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 Db AAAGAAGCACCTTGGGAATATCAGAAACGCCACACAGCCTGCCCCCATGAAGAGTG 3235  
 3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCACACAGCCTGCCCCCATGAAGAGTG 3235  
 3121 ATAATCTTTGCAATGTGAACCTTCACTGACAGTCCAGTCCAGTGGGCTCTGGTACTGAGCAT 3180  
 Db ATAATCTTTGCAATGTGAACCTTCACTGACAGTCCAGTCCAGTGGGCTCTGGTACTGAGCAT 3295  
 3236 ATAATCTTTGCAATGTGAACCTTCACTGACAGTCCAGTCCAGTGGGCTCTGGTACTGAGCAT 3295  
 3181 CTGACAGCACTCATTAATCAAGAAAGGTGGCATTTGGGAAGAACCGGAGCTGGA 3240  
 Db CTGACAGCACTCATTAATCAAGAAAGGTGGCATTTGGGAAGAACCGGAGCTGGA 3355  
 3296 CTGACAGCACTCATTAATCAAGAAAGGTGGCATTTGGGAAGAACCGGAGCTGGA 3355  
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 3356 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTGAGAACCGGAGTAAATTTGGATT 3415  
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 3361 CCTCAGGAACCTGTTTGTCTCACTGGAACTAGGAAACCTGGATCCCTTTAAATGAG 3420  
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 3476 CCTCAGGAACCTGTTTGTCTCACTGGAACTAGGAAACCTGGATCCCTTTAAATGAG 3535  
 3421 CACACGATGAGGAACTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA 3480  
 Db CACACGATGAGGAACTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA 3595  
 3481 GATCTTCTGTGTAATGATGATGAAATAGCAGAACTCAGATCCAAATTTAGTGTGGA 3540  
 Db GATCTTCTGTGTAATGATGATGAAATAGCAGAACTCAGATCCAAATTTAGTGTGGA 3655  
 3596 GATCTTCTGTGTAATGATGATGAAATAGCAGAACTCAGATCCAAATTTAGTGTGGA 3655  
 3541 CAAGAACAACCTGGTGCCTTCCAGGCAATCTCAGGAAATCAGATATTCATATT 3600  
 Db CAAGAACAACCTGGTGCCTTCCAGGCAATCTCAGGAAATCAGATATTCATATT 3715  
 3656 CAAGAACAACCTGGTGCCTTCCAGGCAATCTCAGGAAATCAGATATTCATATT 3715  
 3601 GATGAAGCGACGGCAATGTGGATCCAAGAACTGATGATGTTTAATAAATAAATAATCCGG 3660  
 Db GATGAAGCGACGGCAATGTGGATCCAAGAACTGATGATGTTTAATAAATAAATAATCCGG 3775  
 3716 GATGAAGCGACGGCAATGTGGATCCAAGAACTGATGATGTTTAATAAATAAATAATCCGG 3775  
 3661 GAGAAATTTGCCACTGACCGTGTCAACCTTCAAGATGTTGCAACCACTGGGCAAGCGAGAA 3720  
 Db GAGAAATTTGCCACTGACCGTGTCAACCTTCAAGATGTTGCAACCACTGGGCAAGCGAGAA 3835  
 3776 GAGAAATTTGCCACTGACCGTGTCAACCTTCAAGATGTTGCAACCACTGGGCAAGCGAGAA 3835  
 3721 AGCCACAAGATAATGTTTGTAGATTCAGGAAGATGGAAGAAATGATGAGCCGTATGTT 3780  
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 3836 AGCCACAAGATAATGTTTGTAGATTCAGGAAGATGGAAGAAATGATGAGCCGTATGTT 3895  
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 Db TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGTTGCAACCACTGGGCAAGCGAGAA 3955  
 3896 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGTTGCAACCACTGGGCAAGCGAGAA 3955  
 3841 GCGCTGCGCTTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 3900  
 Db GCGCTGCGCTTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4015  
 3956 GCGCTGCGCTTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4015  
 3901 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGAGACCGCTCGACCTTAACTATT 3960  
 Db GGTCACTGACCACTGGTTTACAAACACTTCCAAATGAGACCGCTCGACCTTAACTATT 4075  
 4016 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGAGACCGCTCGACCTTAACTATT 4075  
 3961 TTCGAGACAGCACTGTGA 3978

Db 4076 TTCGAGACAGCACTGTGA 4093  
 RESULT 8  
 AAH81778  
 ID AAH81778 standard; DNA; 4231 BP.  
 XX  
 AC AAH81778;  
 XX  
 DT 21-SEP-2001 (first entry)  
 XX  
 DE Human differential transcription-associated cDNA SEQ ID 287.  
 XX  
 KW Differential transcription; human; rat; tumour cell; cytostatic;  
 KW Ras modulator; Class II tumour suppressor gene; gene therapy; sa.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200157058-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 31-JAN-2001; 2001WO-EP001003.  
 XX  
 PR 31-JAN-2000; 2000DE-01004102.  
 XX  
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 XX  
 PI Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;  
 PI Grips M, Heilriegel M, Schmitz A, Sers C;  
 XX  
 DR WPI; 2001-483415/52.  
 XX  
 PT Nucleic acids differentially expressed between tumor and normal cells,  
 PT useful for diagnosis or therapy of tumors and for screening active  
 PT agents.  
 XX  
 PS Disclosure; Page 442-443; 579pp; German.  
 XX  
 CC This invention describes a nucleic acid (I) with differential expression  
 CC between tumor and normal cells and which has cytostatic activity. (I)  
 CC work as modulators of Ras activity by inducing expression of tumour  
 CC suppressor genes. (I), and polypeptides encoded by them, are useful as  
 CC targets for diagnosis or therapy and in screening to determine the  
 CC effects of an active compound (potential pharmaceutical) on a cell line,  
 CC particularly for diagnosis and treatment of tumors, especially by  
 CC modulating expression of (I) (by gene therapy, antisense RNA or ribozyme  
 CC methods) or by modulating the amount and/or location of (I)-encoded  
 CC polypeptides (by administration of the polypeptide or its activator,  
 CC antibody (optionally as a conjugate) or inhibitor). The method allows  
 CC identification of many Class II tumour suppressor genes (i.e. genes that  
 CC are not primary targets for tumour-initiating mutations). AAH81492-  
 CC AAH82376 represent the human and rat derived nucleic acid fragments  
 CC described in the method of the invention  
 XX  
 SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;  
 Query Match 99.9%; Score 3973.2; DB 5; Length 4231;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ATGCTGCCCGTGTACACGAGGAGTGAAGCCCAACCCGCTGCAGGACGGAACCTCTGCTCA 60  
 Db 116 ATGCTGCCCGTGTACACGAGGAGTGAAGCCCAACCCGCTGCAGGACGGAACCTCTGCTCA 175  
 QY 61 CGCGTGTCTTCTGCTGGCTCAATCCCTTGTGTTTAAATTTGGCCATAAACGGAGATTAGAG 120  
 Db 176 CGCGTGTCTTCTGCTGGCTCAATCCCTTGTGTTTAAATTTGGCCATAAACGGAGATTAGAG 235  
 QY 121 GAAGATGATATGATTTTCAAGTGTGCTGCCAGAGAACCGCTGCACAGCACTTTGGAGAGAGTTG 180  
 Db 236 GAAGATGATATGATTTTCAAGTGTGCTGCCAGAGAACCGCTGCACAGCACTTTGGAGAGAGTTG 295





PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-0358809P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.  
PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
XX  
XX WPI; 2003-468649/44.  
DR P-PSDB; ADN39254.  
XX  
PT Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.  
XX  
PS Claim 8; SEQ ID NO 571; 1385pp; English.  
XX  
XX The invention relates to nucleic acids and proteins (ADN38693-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularization syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a nucleic acid sequence of the invention.  
XX  
XX Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;  
SQ

Query Match 99.9%; Score 3973.2; DB 11; Length 4231;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCTGCCGTGTACCAGGAGTGAAGCCCAACCGCTGCGAGGACGGAACTCTGCTCA 60  
Db 116 ATGCTGCCGTGTACCAGGAGTGAAGCCCAACCGCTGCGAGGACGGAACTCTGCTCA 175

Qy 61 CGCGTGTCTTCTGGTGCTCAATCCCTTGTAAATTTGGCCATAAAGGAGATTAGAG 120  
Db 176 CGCGTGTCTTCTGGTGCTCAATCCCTTGTAAATTTGGCCATAAAGGAGATTAGAG 235

Qy 121 GAAGATGATATGATATTCAGTCTGCGAGAAAGCCGCTCAGACACCTTTGGAGAGAGTTG 180  
Db 236 GAAGATGATATGATATTCAGTCTGCGAGAAAGCCGCTCAGACACCTTTGGAGAGAGTTG 295

Qy 181 CAAGGTTCTGGATAAGAGATTTTAAGACTGAGATGACGACGAGCCCTTCTTTA 240  
Db 296 CAAGGTTCTGGATAAGAGATTTTAAGACTGAGATGACGACGAGCCCTTCTTTA 355

Qy 241 ACAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTAGTTTGGGAATTTTACGTGA 300  
Db 356 ACAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTAGTTTGGGAATTTTACGTGA 415

Qy 301 ATTGAGGAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAAAATTTATTAATTTT 360  
Db 416 ATTGAGGAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAAAATTTATTAATTTT 475

Qy 361 GAAAAATTATGATCCCATGGATTCTGTGGCTTTGAAACACAGCTACGCTATGCCACGGTG 420  
Db 476 GAAAAATTATGATCCCATGGATTCTGTGGCTTTGAAACACAGCTACGCTATGCCACGGTG 535

Qy 421 CTGACTTTTTGCACGCTCATTTTTGGCTATATCTGCATCACTTATATTTTTATCAGTTCAAG 480  
Db 536 CTGACTTTTTGCACGCTCATTTTTGGCTATATCTGCATCACTTATATTTTTATCAGTTCAAG 595

Qy 481 TGTCTGGGATGAGTTACGAGTAGCCATGTCATATGATTTATCGNAGGCACTTCGT 540  
Db 596 TGTCTGGGATGAGTTACGAGTAGCCATGTCATATGATTTATCGNAGGCACTTCGT 655

Qy 541 CTTAGTAACATGGCCATGGGCAAGACAACACAGGCCAGATAGTCAATCTCTCTGCCAAT 600  
Db 656 CTTAGTAACATGGCCATGGGCAAGACAACACAGGCCAGATAGTCAATCTCTCTGCCAAT 715

Qy 601 GATGTGAACAAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACAGGACCACTG 660  
Db 716 GATGTGAACAAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACAGGACCACTG 775

Qy 661 CAGCGATCGCAGTACTGCCCTACTCTGATGAGATAGGAATATCGTGCCTTCTCTGGG 720  
Db 776 CAGCGATCGCAGTACTGCCCTACTCTGATGAGATAGGAATATCGTGCCTTCTCTGGG 835

Qy 721 ATGSCAGTCTTAATCAATCTCTGCCCTTGCACAAAGCTGTTTGGGAAAGTTGTTCTCATCA 780  
Db 836 ATGSCAGTCTTAATCAATCTCTGCCCTTGCACAAAGCTGTTTGGGAAAGTTGTTCTCATCA 895

Qy 781 CTGAGGAGTAAAACTGCAACTTTTACCGATGCCAGATCAGGACCATGAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAAACTGCAACTTTTACCGATGCCAGATCAGGACCATGAATGAAGTTATA 955

Qy 841 ACTGATATAGGATAATAAANAATGACCTGGGAAAAGTCATTTTCAATCTTATTACC 900  
Db 956 ACTGATATAGGATAATAAANAATGACCTGGGAAAAGTCATTTTCAATCTTATTACC 1015

Qy 901 AATTGAGAAGAGGAGATTTCACAGATTCTGAGAAGTTCTCCCTCAGGGGATGAAT 960  
Db 1016 AATTGAGAAGAGGAGATTTCACAGATTCTGAGAAGTTCTCCCTCAGGGGATGAAT 1075

Qy 961 TTGCTTTCTGTTTTTTCAGTGAAGCAAAATCATCGTGTGTTGTGACCTTCCACCATCAGCTG 1020  
Db 1076 TTGCTTTCTGTTTTTTCAGTGAAGCAAAATCATCGTGTGTTGTGACCTTCCACCATCAGCTG 1135

Qy 1021 CTCCTCGGAGTGTGATCAGCAGCGCGGTGTTCTGTCAGTGAAGCTGTATGGGGCT 1080  
Db 1136 CTCCTCGGAGTGTGATCAGCAGCGCGGTGTTCTGTCAGTGAAGCTGTATGGGGCT 1195

Qy 1081 GTGCGGTGACGGTTACCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1140  
Db 1196 GTGCGGTGACGGTTACCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1255

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Db 1256 GTCAGCATCCGAGAAATCCAGACCTTTTGTACTTGTATGATGATATCACAGCGCAACCGT 1315

Qy 1201 CAGCTGCGTCAGATGTTAAAGATGTCATGTCAGGATTTTACTGCTTTTGGAT 1260  
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Qy 1261 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTACTGTGAGACCTGGGGAATG 1320  
Db 1376 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTACTGTGAGACCTGGGGAATG 1435

Qy 1321 TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCATCACTGTTTAAGTCCGCTGCTCGG 1380  
Db 1436 TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCATCACTGTTTAAGTCCGCTGCTCGG 1495

Qy 1381 GAATTTGCCCAAGTCAGGGCTGTCAGCTGATGGAAGATTTGCTATGCTCTCAG 1440  
Db 1496 GAATTTGCCCAAGTCAGGGCTGTCAGCTGATGGAAGATTTGCTATGCTCTCAG 1555

Qy 1441 CAGCCCTGGGTGTTCTCGGGAACTCTCGAGGAGTAAATATTTTATTTGGGAGAAATA CGAA 1500

Db 1556 ||||| CAGCCCTGGGTCTCTCGGAACTCTGAGGAGTAATATTTATTTTGGGAAGAAATATGAA 1615  
Qy 1501 AAGGAACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1560  
Db 1616 AAGGAACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675  
Qy 1561 GAGGATGATCTGATCTGTGATAGGAGATCGGGAACCAACGCTGAGTGGAGGCGAGAAA 1620  
Db 1676 GAGGATGATCTGATCTGTGATAGGAGATCGGGAACCAACGCTGAGTGGAGGCGAGAAA 1735  
Qy 1621 GCAGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGATCTATCTCTGAGCAGAT 1680  
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Qy 1681 CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGATTTGTCAA 1740  
Db 1796 CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGATTTGTCAA 1855  
Qy 1741 ATTTTGCATGAGAAGATCACAAATTTTAGTGACTCATCAAGTTGCAGTACCTCAAAGCTGCA 1800  
Db 1856 ATTTTGCATGAGAAGATCACAAATTTTAGTGACTCATCAAGTTGCAGTACCTCAAAGCTGCA 1915  
Qy 1801 AGTCAGATTTCTGATATTTGAAGATGTTAAATGTTGCGAAGGGGACCTTACCTGAGTTTC 1860  
Db 1916 AGTCAGATTTCTGATATTTGAAGATGTTAAATGTTGCGAAGGGGACCTTACCTGAGTTTC 1975  
Qy 1861 CTAAAACTCTGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 1920  
Db 1976 CTAAAACTCTGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACTTCTCAGAGTCTTCGTTTGG 1980  
Db 2036 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACTTCTCAGAGTCTTCGTTTGG 2095  
Qy 1981 TCTCAACAACTTCTAGACCCTCTTGAAGATGTTGCTCTGGAGAGCCAAAGATACAGAG 2040  
Db 2096 TCTCAACAACTTCTAGACCCTCTTGAAGATGTTGCTCTGGAGAGCCAAAGATACAGAG 2155  
Qy 2041 AATGTCAGGTTACACTATCAGAGAGAACCGTTCTGAAGGAAAGTTGGTTTTAGGCC 2100  
Db 2156 AATGTCAGGTTACACTATCAGAGAGAACCGTTCTGAAGGAAAGTTGGTTTTAGGCC 2215  
Qy 2101 TATAAGAAATTAATTCAGAGCTGGTCTCAGCTGATGTTCTTCAATTTCTTATTTCTCTTA 2160  
Db 2216 TATAAGAAATTAATTCAGAGCTGGTCTCAGCTGATGTTCTTCAATTTCTTATTTCTCTTA 2275  
Qy 2161 AACACTGAGCTCAGGTTGCCCTATGCTTCAAGATGTTGGCTTTTCATCTGGGCAAC 2220  
Db 2276 AACACTGAGCTCAGGTTGCCCTATGCTTCAAGATGTTGGCTTTTCATCTGGGCAAC 2335  
Qy 2221 AAACAAAGTATGCTAAATGTCACCTGTAATCGAGGAGGAATGTAAACGAGAACTAGAT 2280  
Db 2336 AAACAAAGTATGCTAAATGTCACCTGTAATCGAGGAGGAATGTAAACGAGAACTAGAT 2395  
Qy 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2340  
Db 2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2455  
Qy 2341 GCAAGATCTCTATTGGTATTCTACGTCCTGTTAACTCTTCAACAACTTTGCAACAAA 2400  
Db 2456 GCAAGATCTCTATTGGTATTCTACGTCCTGTTAACTCTTCAACAACTTTGCAACAAA 2515  
Qy 2401 ATGTTTTCAGTCAATTTCTGAAGCTCCGGTATTATTTCTTGTATAGAAATCCAAATAGGAAGA 2460  
Db 2516 ATGTTTTCAGTCAATTTCTGAAGCTCCGGTATTATTTCTTGTATAGAAATCCAAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCAAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTCAGCTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCAAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTCAGCTTT 2635  
Qy 2521 TTAGATTTCAATCCAGACATTTGCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2580  
|||||

Db 2636 TTAGATTTCAATCCAGACATTTGCTACAAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2695  
Qy 2581 ATTCCTTGGATCGAAATACCCCTTGGTTCCTCTTGAATCATTTTCATTTTCTTCGGGGA 2640  
Db 2696 ATTCCTTGGATCGAAATACCCCTTGGTTCCTCTTGAATCATTTTCATTTTCTTCGGGGA 2755  
Qy 2641 TATTTTGGAAAACTCAAGAGATGTGAAGCCCTGGAAATCTACAACTCGGAGTCCAGTG 2700  
Db 2756 TATTTTGGAAAACTCAAGAGATGTGAAGCCCTGGAAATCTACAACTCGGAGTCCAGTG 2815  
Qy 2701 TTTTCCCACTTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760  
Db 2816 TTTTCCCACTTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875  
Qy 2761 GAGAGTGTCAAGAACTGTTTGTATGTCACACAGAGATTTACATTCAGAGGCTTGGTCTTG 2820  
Db 2876 GAGAGTGTCAAGAACTGTTTGTATGTCACACAGAGATTTACATTCAGAGGCTTGGTCTTG 2935  
Qy 2821 TTTTGGACAACTCCCGTGGTCCCGTCTGGATGCCATCTGTGCCATGTTTGT 2880  
Db 2936 TTTTGGACAACTCCCGTGGTCCCGTCTGGATGCCATCTGTGCCATGTTTGT 2995  
Qy 2881 ATCATGTTGGCTTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 2940  
Db 2996 ATCATGTTGGCTTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 3055  
Qy 2941 TTGGCACTGTCCTATGCTCCACGCTCATGGGATGTTTTCAGTGGTGTTCGACAAAGT 3000  
Db 3056 TTGGCACTGTCCTATGCTCCACGCTCATGGGATGTTTTCAGTGGTGTTCGACAAAGT 3115  
Qy 3001 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAAAGGTCATTGAAATACACAGACCTTGA 3060  
Db 3116 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAAAGGTCATTGAAATACACAGACCTTGA 3175  
Qy 3061 AAAGAACACCTTGGGAATATCAGAAACGCCCAACACAGCCTGGCCCCATGAAGAGTG 3120  
Db 3176 AAAGAACACCTTGGGAATATCAGAAACGCCCAACACAGCCTGGCCCCATGAAGAGTG 3235  
Qy 3121 ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTCTGTAATGAAGAT 3180  
Db 3236 ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTCTGTAATGAAGAT 3295  
Qy 3181 CTGACAGCACTCAATTAATCAAGAAAAAGTTGGCAATTTGGGAAGAACCCGAGCTGGA 3240  
Db 3296 CTGACAGCACTCAATTAATCAAGAAAAAGTTGGCAATTTGGGAAGAACCCGAGCTGGA 3355  
Qy 3241 AAAAGTTCCTCATCTCAGCCCTTTTAGATTGTACAGAACCCGAAAGGTAAATTTGGATT 3300  
Db 3356 AAAAGTTCCTCATCTCAGCCCTTTTAGATTGTGTACAGAACCCGAAAGGTAAATTTGGATT 3415  
Qy 3301 GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAGGAAGAAATGTCATCATATA 3360  
Db 3416 GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAGGAAGAAATGTCATCATATA 3475  
Qy 3361 CCTCAGGAACCTGTTTTTGTTCACCTGGAAACATAGAGGAAAAACCTTGGATCCCTTTAATCAG 3420  
Db 3476 CCTCAGGAACCTGTTTTTGTTCACCTGGAAACATAGAGGAAAAACCTTGGATCCCTTTAAGGAG 3535  
Qy 3421 CACACGATGAGGAACCTGTGGATGTCCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3480  
Db 3536 CACACGATGAGGAACCTGTGGATGTCCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3595  
Qy 3481 GATCTTCTCGTAAAAATGGATACGTAATAGCAGAAATCAGGATCCAAATTTTAGTGTGGA 3540  
Db 3596 GATCTTCTCGTAAAAATGGATACGTAATAGCAGAAATCAGGATCCAAATTTTAGTGTGGA 3655  
Qy 3541 CAAAGACAACTGGTGTCCCTTGCAGGGCAATTTCTCAGGAAAAATCAGATATGATTAAT 3600  
Db 3656 CAAAGACAACTGGTGTCCCTTGCAGGGCAATTTCTCAGGAAAAATCAGATATGATTAAT 3715  
Qy 3601 GATGAAGCGACGGCAATGTGGATCCAAAGATCTGATGAGTTAATACAAAAAATCCGG 3660  
Db 3716 GATGAAGCGACGGCAATGTGGATCCAAAGATCTGATGAGTTAATACAAAAAATCCGG 3775  
|||||



QY 3661 GAGAAATTCGCCACTGCACGCTGCTAACCAATTCGACACAGATTGACACCATTAATGAC 3720  
 Db 3776 GAGAAATTCGCCACTGCACGCTGCTAACCAATTCGACACAGATTGACACCATTAATGAC 3835  
 QY 3721 AGCGACAAGATAATGGTTTATGATTACAGGAACTGAAAGATATGATGAGCCGTATGTT 3780  
 Db 3836 AGCGACAAGATAATGGTTTATGATTACAGGAACTGAAAGATATGATGAGCCGTATGTT 3895  
 QY 3781 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGTTGCAACAATCTGGGCAAGGCAGAA 3840  
 Db 3896 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGTTGCAACAATCTGGGCAAGGCAGAA 3955  
 QY 3841 GCCCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATATCCACATATT 3900  
 Db 3956 GCCCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATATCCACATATT 4015  
 QY 3901 GGTCACTGACCACTGGTTTACAAACATCTTCCAAATGGACAGCCCTCGACCTTAACATATT 3960  
 Db 4016 GGTCACTGACCACTGGTTTACAAACATCTTCCAAATGGACAGCCCTCGACCTTAACATATT 4075  
 QY 3961 TTCGAGACAGCACTGTGA 3978  
 Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 10  
 ADR66822  
 ID ADR66822 standard; DNA; 5832 BP.  
 XX ADR66822;  
 AC ADR66822;  
 DT 02-DEC-2004 (first entry)  
 XX Human prostatic carcinoma derived DNA SEQ ID 115 #4.  
 DE human; cytostatic; diagnosis; prostatic cancer;  
 KW differential expression analysis; ds.  
 OS Homo sapiens.  
 XX WO2004076614-A2.  
 PN 10-SEP-2004.  
 PD 22-FEB-2004; 2004WO-DE000433.  
 PP 27-FEB-2003; 2003DE-01009985.  
 PR 14-MAY-2003; 2003DE-01022134.  
 XX (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (ROSE/) ROSENTHAL A.  
 PA (HERM/) HERMANN K.  
 PA (PILA/) PILARSKY C.  
 XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pillarsky C, Specht T;  
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
 PI Xinzhang L, Staub E;  
 XX WPI; 2004-653386/63.  
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
 PT useful for diagnosis, treatment and in screening for specific binding  
 PT agents.  
 XX Claim 1; Page 1348-1349; 1607pp; German.  
 CC This invention describes novel cytostatic polynucleotide and polypeptide  
 CC sequences which can be used in a method for diagnosing prostatic cancer  
 CC or the risk of developing prostatic cancer. Diagnosis is based on  
 CC determining over transcription or over expression of the sequences in  
 CC prostatic tissue. Screening for inhibitors of the sequences or detection

CC substances involves a binding assay, any compounds that bind are  
 CC selected, optionally after deconvolution of mixtures. Detection of a  
 CC predetermined minimum level of the reporter indicates the presence of  
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
 CC short-interfering RNA or ribozymes; an organic molecule of molecular  
 CC weight below 5000, preferably 300, that binds to the polypeptide; an  
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
 CC (monoclonal) antibody directed against Ab or any of the above derivatised  
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
 CC radioisotope. The polynucleotides are identified in human prostatic  
 CC cancer by differential expression analysis, using DNA microarrays,  
 CC between normal and tumorous tissues, with (over)expression being detected  
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
 CC prostatic cancer patients, or subjects at risk, were incubated  
 CC sequentially with anti-human CD4 murine monoclonal antibodies;  
 CC biotinylated second antibody; streptavidin-conjugated horseradish  
 CC peroxidase and then diaminobenzidine as colour former (brown). The  
 CC samples were counterstained with hemalum (blue). Malignant cells stained  
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
 CC lymph node metastases were also stained. ADR65805-ADR6594 represent the  
 CC polynucleotide and polypeptide sequences used in the method of the  
 CC invention.

XX SQ Sequence 5832 BP; 1660 A; 1175 C; 1306 G; 1691 T; 0 U; 0 Other;  
 Query Match 99.9%; Score 3973.2; DB 13; Length 5832;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ATGCTGCCCGTGTACAGGAGGTGAAGCCCAACCGCTGCAGGACGGAACCTTGCTCA 60  
 Db 116 ATGCTGCCCGTGTACAGGAGGTGAAGCCCAACCGCTGCAGGACGGAACCTTGCTCA 175  
 QY 61 CGCGTGTCTTCGTGGCTCAATCCCTCTGTTTAAATTTGCCATAAAGGAGATTAGAG 120  
 Db 176 CGCGTGTCTTCGTGGCTCAATCCCTCTGTTTAAATTTGCCATAAAGGAGATTAGAG 235  
 QY 121 GAAGATGATATGATTCAGTCTGCCAAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180  
 Db 236 GAAGATGATATGATTCAGTCTGCCAAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 295  
 QY 181 CAAGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGATGAGAGAGCTTCTTTA 240  
 Db 296 CAAGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGATGAGAGAGCTTCTTTA 355  
 QY 241 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAATTTTACGTTA 300  
 Db 356 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAATTTTACGTTA 415  
 QY 301 ATTGAGGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTT 360  
 Db 416 ATTGAGGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTT 475  
 QY 361 GAAATATGATCCCATGATCTCTGGCTTTGAAACAGAGCTAGCTATGCCACGGTG 420  
 Db 476 GAAATATGATCCCATGATCTCTGGCTTTGAAACAGAGCTAGCTATGCCACGGTG 535  
 QY 421 CTGACTTTTTCGACGCTCATTTTGGCTTACTGTCATCACTTATATTTTATCAGTTTCAG 480  
 Db 536 CTGACTTTTTCGACGCTCATTTTGGCTTACTGTCATCACTTATATTTTATCAGTTTCAG 595  
 QY 481 TGTCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 540  
 Db 596 TGTCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655  
 QY 541 CTTAGTAACATGGCCATGGGGAAGACAAACAGCCAGATAGTCAATCTGCTGCTCAAT 600  
 Db 656 CTTAGTAACATGGCCATGGGGAAGACAAACAGCCAGATAGTCAATCTGCTGCTCAAT 715  
 QY 601 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCTGCTGGGAGGACCACTG 660



Db 716 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGTGGCAGGACCACTG 775  
Qy 661 CAGCGCATCGCAGTGACTGCCCTACTCTGGATGAGATAGGAATATCGTGCCTTGTCTGGG 720  
Db 776 CAGCGCATCGCAGTGACTGCCCTACTCTGGATGAGATAGGAATATCGTGCCTTGTCTGGG 835  
Qy 721 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 780  
Db 836 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 895  
Qy 781 CTGAGGAGTAAACTGCACTTTACCGATGCCAGATCAGGACCATGAATGAATTATA 840  
Db 896 CTGAGGAGTAAACTGCACTTTACCGATGCCAGATCAGGACCATGAATGAATTATA 955  
Qy 841 ACTGGTATAAGGATAATAAAATGTAGCCCTGGGAAAAGTCATTTCAAATCTTATTACC 900  
Db 956 ACTGGTATAAGGATAATAAAATGTAGCCCTGGGAAAAGTCATTTCAAATCTTATTACC 1015  
Qy 901 AATTGTGAAGAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTGCTCTCAGGGGATGAAT 960  
Db 1016 AATTGTGAAGAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTGCTCTCAGGGGATGAAT 1075  
Qy 961 TTGGCTTCGTTTTACGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCAACCTACGTG 1020  
Db 1076 TTGGCTTCGTTTTACGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCAACCTACGTG 1135  
Qy 1021 CTCCTCGCAGTGTGATCACAGCCAGCCGGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080  
Db 1136 CTCCTCGCAGTGTGATCACAGCCAGCCGGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195  
Qy 1081 GTGCGGTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1140  
Db 1196 GTGCGGTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1255  
Qy 1141 GTGAGCATCCGAGAAATCCAGACCTTTTGTGCTACTTGATGAGATATCACAGCGCAACCGT 1200  
Db 1256 GTGAGCATCCGAGAAATCCAGACCTTTTGTGCTACTTGATGAGATATCACAGCGCAACCGT 1315  
Qy 1201 CAGCTCCGTCAGATGTGTAAGAAAGATGTCATGTGCGAGGATTTACTGCTTTTGGGAT 1260  
Db 1316 CAGCTCCGTCAGATGTGTAAGAAAGATGTCATGTGCGAGGATTTACTGCTTTTGGGAT 1375  
Qy 1261 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTCTTTACTGTGACACCTGCGCAATTG 1320  
Db 1376 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTCTTTACTGTGACACCTGCGCAATTG 1435  
Qy 1321 TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTAAAGTCCGCTGCTCGG 1380  
Db 1436 TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTAAAGTCCGCTGCTCGG 1495  
Qy 1381 GAATTGSCCCCAAGTCAAGGCTGGTCAGCGTGATCGAGAAATGCTGCTATGTCTCAG 1440  
Db 1496 GAATTGSCCCCAAGTCAAGGCTGGTCAGCGTGATCGAGAAATGCTGCTATGTCTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGNACTCTCAGGAGTAATAATTTTATTTGGGAAGAAATACGA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGNACTCTCAGGAGTAATAATTTTATTTGGGAAGAAATAGAA 1615  
Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTTG 1560  
Db 1616 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTTG 1675  
Qy 1561 GAGGATGGTGTGATGATAGGATGCGGGACCAAGCTGAGTGGAGGCGAGAAA 1620  
Db 1676 GAGGATGGTGTGATGATAGGATGCGGGACCAAGCTGAGTGGAGGCGAGAAA 1735  
Qy 1621 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATCTGACATCTATCTCTGAGCAT 1680  
Db 1736 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATCTGACATCTATCTCTGAGCAT 1795  
Qy 1681 CCTCTCAGTCAGTGTGAGTGGGAAGTTAGCAGACACTGTTTCGAACCTGTGTTTGTCAA 1740

Db 1796 CCTCTCAGTCGATGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTTGTCAA 1855  
Qy 1741 ATTTTGCATCAGAGAATCACAATTTTGTAGTCACTCATCAGTTGCACTACCTCAAAAGCTGCA 1800  
Db 1856 ATTTTGCATCAGAGAATCACAATTTTGTAGTCACTCATCAGTTGCACTACCTCAAAAGCTGCA 1915  
Qy 1801 AGTCAGATTCGTATTTTGAAGATGTTAAATGTTGTCAGAAAGGGAATTAACACTGAGTTC 1860  
Db 1916 AGTCAGATTCGTATTTTGAAGATGTTAAATGTTGTCAGAAAGGGAATTAACACTGAGTTC 1975  
Qy 1861 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATATGAGGAAGTGAACAA 1920  
Db 1976 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATATGAGGAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGGTTTGG 1980  
Db 2036 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGGTTTGG 2095  
Qy 1981 TCTCAACAATCTTCTAGACCTCTTGAAGATGTTGCTCTGGAGAGCCAAAGATACAGAG 2040  
Db 2096 TCTCAACAATCTTCTAGACCTCTTGAAGATGTTGCTCTGGAGAGCCAAAGATACAGAG 2155  
Qy 2041 AATGTCCCAGTTACACTATCAGAGGAAACCGTCTGAAGGAAGTGGTTTTCAGGCC 2100  
Db 2156 AATGTCCCAGTTACACTATCAGAGGAAACCGTCTGAAGGAAGTGGTTTTCAGGCC 2215  
Qy 2101 TATAAGAAATTAATCAGAGTGGTGTCTCTGGAATGTCTTCAATTTCTTATTTCTCTTA 2160  
Db 2216 TATAAGAAATTAATCAGAGTGGTGTCTCTGGAATGTCTTCAATTTCTTATTTCTCTTA 2275  
Qy 2161 AACACTGCACTCAGGTTGCTATGTCTTCAAGATGTTGGTCTTCACTACTGGGCAAA 2220  
Db 2276 AACACTGCACTCAGGTTGCTATGTCTTCAAGATGTTGGTCTTCACTACTGGGCAAA 2335  
Qy 2221 AACAAAGTATGTAATGTCACTGTAATGAGGAGGAATGTAAACGAGAGCTAGAT 2280  
Db 2336 AACAAAGTATGTAATGTCACTGTAATGAGGAGGAATGTAAACGAGAGCTAGAT 2395  
Qy 2281 CTTAACTGGTACTAGGAATTTTATTCAGGTTTAACTGTAGTACCGTCTTTTGGGATA 2340  
Db 2396 CTTAACTGGTACTAGGAATTTTATTCAGGTTTAACTGTAGTACCGTCTTTTGGGATA 2455  
Qy 2341 GCAAGATCTCTATTTGGTATTTCTACGTCCTTGTAACTTTTCAACAACTTTGCAACAAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTACGTCCTTGTAACTTTTCAACAACTTTGCAACAAA 2515  
Qy 2401 ATGTTTGAATCAATCTGAAGCTCCGGTATTTCTTTGATAGAAATCCAATAGGAAGA 2460  
Db 2516 ATGTTTGAATCAATCTGAAGCTCCGGTATTTCTTTGATAGAAATCCAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCGCTGACGTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCGCTGACGTTT 2635  
Qy 2521 TTAGATTTTCAATCAGACATTTGCTACAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2580  
Db 2636 TTAGATTTTCAATCAGACATTTGCTACAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2695  
Qy 2581 ATTCTTGGATCCGAATACCCTTGGTTCCTTGGGAATCAATTTTCAATTTTCTTTCGCGGA 2640  
Db 2696 ATTCTTGGATCCGAATACCCTTGGTTCCTTGGGAATCAATTTTCAATTTTCTTTCGCGGA 2755  
Qy 2641 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGAATCTCAACCTCGGAGTCCAAGT 2700  
Db 2756 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGAATCTCAACCTCGGAGTCCAAGT 2815  
Qy 2701 TTTTCCCACTTGTCACTCTCTCCAGGGGCTCTGGACCACTCCGGGCATACAAAGCAGAA 2760  
Db 2816 TTTTCCCACTTGTCACTCTCTCCAGGGGCTCTGGACCACTCCGGGCATACAAAGCAGAA 2875  
Qy 2761 GAGAGGTGTGAGAACTGTTTGTATGACACACAGATTTTACATTCAGAGGCTGTGTTCTTG 2820  
Db 2876 GAGAGGTGTGAGAACTGTTTGTATGACACACAGATTTTACATTCAGAGGCTGTGTTCTTG 2935

Qy 2821 TTTTGGCAACGTCCTCGCTGGTTCGCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTG 2880  
 Db 2936 TTTTGGCAACGTCCTCGCTGGTTCGCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTG 2995  
 Qy 2881 ATCATCGTTGCTTGGGTCCTCGATCTGCGCAAAATCTCGGATGCGCGCAGGTTGGT 2940  
 Db 2996 ATCATCGTTGCTTGGGTCCTCGATCTGCGCAAAATCTCGGATGCGCGCAGGTTGGT 3055  
 Qy 2941 TTGGCATGTCCTATGCGCTCATGCGGAGTGTTCAGTGGTGTGTTCGACAAAGT 3000  
 Db 3056 TTGGCATGTCCTATGCGCTCATGCGGAGTGTTCAGTGGTGTGTTCGACAAAGT 3115  
 Qy 3001 GCTGAAGTGGATATGATGATCTCATGTAAGAGGTCATTTGATATACACAGACTTGAA 3060  
 Db 3116 GCTGAAGTGGATATGATGATCTCATGTAAGAGGTCATTTGATATACACAGACTTGAA 3175  
 Qy 3061 AAGAAGCACCCTGGGAATATCAGAAACGCCACACAGCCTGCGCCCATGAAGAGTG 3120  
 Db 3176 AAGAAGCACCCTGGGAATATCAGAAACGCCACACAGCCTGCGCCCATGAAGAGTG 3235  
 Qy 3121 ATAATCTTGAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3180  
 Db 3236 ATAATCTTGAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3295  
 Qy 3181 CTGACGACACTTAATACACAGAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3240  
 Db 3296 CTGACGACACTTAATACACAGAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355  
 Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTGAGAACCCGAGGTAAATTTGGATT 3300  
 Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTGAGAACCCGAGGTAAATTTGGATT 3415  
 Qy 3301 GATAAGATCTTGAACATGAATTTGACTTACGATTTAAGGAAGAAATGTCAATCAT 3360  
 Db 3416 GATAAGATCTTGAACATGAATTTGACTTACGATTTAAGGAAGAAATGTCAATCAT 3475  
 Qy 3361 CCTCAGAACCTGTTTGTTCACCTGGACATGAGGAACCTGGATCCCTTTAAGTGA 3420  
 Db 3476 CCTCAGAACCTGTTTGTTCACCTGGACATGAGGAACCTGGATCCCTTTAAGTGA 3535  
 Qy 3421 CACACGATGAGGAACCTGTTGAAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA 3480  
 Db 3536 CACACGATGAGGAACCTGTTGAAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA 3595  
 Qy 3481 GATCTTCTGTGTAATGATGATGTAATTAGCAGATCCAAATTTAGTGTGGA 3540  
 Db 3596 GATCTTCTGTGTAATGATGATGTAATTAGCAGATCCAAATTTAGTGTGGA 3655  
 Qy 3541 CAAAGCAACTGTTGCTTGCCTGCGGCAATTTCTCAGGAATAATCAGATATGATTTATT 3600  
 Db 3656 CAAAGCAACTGTTGCTTGCCTGCGGCAATTTCTCAGGAATAATCAGATATGATTTATT 3715  
 Qy 3601 GATGAAGCGACGCAAAATGTGGATCCAGAACTGATGATTAATACAAAAAATCCGG 3660  
 Db 3716 GATGAAGCGACGCAAAATGTGGATCCAGAACTGATGATTAATACAAAAAATCCGG 3775  
 Qy 3661 GAGAAATTTGCCCATGCGCTGCTAACCATGTCACAGATTTGAACCATTTATTGAC 3720  
 Db 3776 GAGAAATTTGCCCATGCGCTGCTAACCATGTCACAGATTTGAACCATTTATTGAC 3835  
 Qy 3721 AGCCACAAGATTAATGTTTGTAGATTTCAGGAGACTGGAAGATATGATGACCCGTATGTT 3780  
 Db 3836 AGCCACAAGATTAATGTTTGTAGATTTCAGGAGACTGGAAGATATGATGACCCGTATGTT 3895  
 Qy 3781 TTGCTGCAAAATAAGAGAGCTATTTTACAAAGTGTGTCACAACTGGGCAAGCGAGAA 3840  
 Db 3896 TTGCTGCAAAATAAGAGAGCTATTTTACAAAGTGTGTCACAACTGGGCAAGCGAGAA 3955  
 Qy 3841 GCCGCTGCCCTCATGTAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCATATT 3900  
 Db 3956 GCCGCTGCCCTCATGTAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCATATT 4015

Qy 3901 GGTCACTGACACATGGTTCAAAACATCTTCAATGGACAGCCTCGACCTTAACTATT 3960  
 Db 4016 GGTCACTGACACATGGTTCAAAACATCTTCAATGGACAGCCTCGACCTTAACTATT 4075  
 Qy 3961 TTCGAGACACACTGTGA 3978  
 Db 4076 TTCGAGACACACTGTGA 4093

RESULT 11  
 ADR65919  
 ID ADR65919 standard; DNA; 5832 BP.  
 XX ADR65919;  
 AC ADR65919;  
 XX 02-DEC-2004 (first entry)  
 DT 02-DEC-2004 (first entry)  
 DE Human prostatic carcinoma derived DNA SEQ ID 115 #1.  
 KW human; cytostatic; diagnosis; prostatic cancer;  
 KW differential expression analysis; ds.  
 OS Homo sapiens.  
 XX Homo sapiens.  
 PN WO2004076614-A2.  
 XX 10-SEP-2004.  
 PD 10-SEP-2004.  
 XX 22-FEB-2004; 2004WO-DE000433.  
 XX 27-FEB-2003; 2003DE-01009985.  
 PR 14-MAY-2003; 2003DE-01022134.  
 XX (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (ROSE/) ROSENTHAL A.  
 PA (HERM/) HERMANN K.  
 PA (PILA/) PILARSKY C.  
 XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
 PI Xinzhong L, Staub E;  
 XX WPI; 2004-653386/63.  
 DR WPI; 2004-653386/63.  
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
 PT useful for diagnosis, treatment and in screening for specific binding  
 PT agents.  
 XX Claim 1; Page 177-178; 1607pp; German.  
 PS This invention describes novel cytostatic polynucleotide and polypeptide  
 XX sequences which can be used in a method for diagnosing prostatic cancer  
 CC or the risk of developing prostatic cancer. Diagnosis is based on  
 CC determining over transcription or over expression of the sequences in  
 CC prostatic tissue. Screening for inhibitors of the sequences or detection  
 CC substances involves a binding assay, any compounds that bind are  
 CC selected, optionally after deconvolution of mixtures. Detection of a  
 CC predetermined minimum level of the reporter indicates the presence of  
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
 CC short-interfering RNA or ribozymes; an organic molecule of molecular  
 CC weight below 5000, preferably 300, that binds to the polypeptide; an  
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
 CC polypeptide, preferably humanised or human; an anti-idiotype, non-human  
 CC (monoclonal) antibody directed against Ab or any of the above derivatised  
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
 CC radioisotope. The polynucleotides are identified in human prostatic  
 CC cancer by differential expression analysis, using DNA microarrays.  
 CC between normal and tumorous tissues, with (over)expression being detected  
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
 CC prostatic cancer patients, or subjects at risk, were incubated  
 CC sequentially with anti-human CD4 murine monoclonal antibodies;

CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then dianiobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly by non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
XX invention.

SQ Sequence 5832 BP; 1660 A; 1175 C; 1306 G; 1691 T; 0 U; 0 Other;

Query Match 99.9%; Score 3973.2; DB 13; Length 5832;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGCTGCCCGTGTAACGAGGTGAAGCCCAACCGCTGCAGGAGCGCAACCTCTGCTCA	60
DB	116	ATGCTGCCCGGTACAGAGGTGAAGCCCAACCGCTGCAGGAGCGCAACCTCTGCTCA	175
QY	61	CGCGTGTCTTCTGCTGCTCAATCCCTGTGTTAAATTTGGCCATAAACGGAGATTAGAG	120
DB	176	CGCGTGTCTTCTGCTGCTCAATCCCTGTGTTAAATTTGGCCATAAACGGAGATTAGAG	235
QY	121	GAAGATGATATGATTTAGTGTGCTGCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG	180
DB	236	GAAGATGATATGATTTAGTGTGCTGCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG	295
QY	181	CAAGGTTCTGGGTAAGAGATTTTAAAGCTGAGATGAGATGAGATGAGATGAGATGAGAT	240
DB	296	CAAGGTTCTGGGTAAGAGATTTTAAAGCTGAGATGAGATGAGATGAGATGAGATGAGAT	355
QY	241	ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA	300
DB	356	ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA	415
QY	301	ATTGAGGAAAGTGCCAAAGTAAATCCAGCCCAATTTTTTGGGAAATTTTAAATTTT	360
DB	416	ATTGAGGAAAGTGCCAAAGTAAATCCAGCCCAATTTTTTGGGAAATTTTAAATTTT	475
QY	361	GAAATATGATCCCATGATCTGTGGCTTTGACAGAGTACGATGATGATGATGATGATGAT	420
DB	476	GAAATATGATCCCATGATCTGTGGCTTTGACAGAGTACGATGATGATGATGATGATGAT	535
QY	421	CTGACTTTTTCAGCTCATTTTGGCTATCTGATCATCTTATTTTATCATCTTTCAG	480
DB	536	CTGACTTTTTCAGCTCATTTTGGCTATCTGATCATCTTATTTTATCATCTTTCAG	595
QY	481	TGCTGCGGATGAGGTTACGATGAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT	540
DB	596	TGCTGCGGATGAGGTTACGATGAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT	655
QY	541	CTTAGTAACATGGCCNTGGGGAAGCAACACAGCCAGATAGTCAATCTGCTGCCAAT	600
DB	656	CTTAGTAACATGGCCNTGGGGAAGCAACACAGCCAGATAGTCAATCTGCTGCCAAT	715
QY	601	GATGTGAACAAGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660
DB	716	GATGTGAACAAGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	775
QY	661	CAGCGCATCGCAGTCACTGCTTCTGAGTGGAGATAGGAATATCGTGCCTTCTGGG	720
DB	776	CAGCGCATCGCAGTCACTGCTTCTGAGTGGAGATAGGAATATCGTGCCTTCTGGG	835
QY	721	ATGCGAGTTCTAATCATCTCTGCTGCTGCAAGAGCTGTTTGGAGAGTTGTTCTCATCA	780
DB	836	ATGCGAGTTCTAATCATCTCTGCTGCTGCAAGAGCTGTTTGGAGAGTTGTTCTCATCA	895
QY	781	CTGAGGAGTAAACTGCAACTTTTACAGATGTCAGGATCAGACCATCAATGAAGTTATA	840
DB	896	CTGAGGAGTAAACTGCAACTTTTACAGATGTCAGGATCAGACCATCAATGAAGTTATA	955
QY	841	ACTGGTATAAGGATAATAAAATGTACGCTCTGGGAAAGTCAATTTTCAAATCTTATTACC	900

DB	956	ACTGGTATAAGGATAATAAAATGTACGCTGGGAAAGTCAATTTTCAAATCTTATTACC	1015
QY	901	AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAGTCTCTGCTCAGGGGGATGAAT	960
DB	1016	AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAGTCTCTGCTCAGGGGGATGAAT	1075
QY	961	TTGCTCTTGGTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCACCACTTACG	1020
DB	1076	TTGCTCTTGGTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCACCACTTACG	1135
QY	1021	CTCCTCGGAGTGTATCAGACGAGCCGCGTGTTCGTGGCAGTGCACCTGTATGGGCT	1080
DB	1136	CTCCTCGGAGTGTATCAGACGAGCCGCGTGTTCGTGGCAGTGCACCTGTATGGGCT	1195
QY	1081	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGCTGTGAGAGCAATC	1140
DB	1196	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGCTGTGAGAGCAATC	1255
QY	1141	GTGAGCATCCGAAGAATCCAGACCTTTTGTCTTGTATGATATCAAGCGCAACCGT	1200
DB	1256	GTGAGCATCCGAAGAATCCAGACCTTTTGTCTTGTATGATATCAAGCGCAACCGT	1315
QY	1201	CAGCTCGGCTCAGATGTTAAAGATGTTGATGTTGATGTTGATGTTGTTGTTGTTG	1260
DB	1316	CAGCTCGGCTCAGATGTTAAAGATGTTGATGTTGATGTTGATGTTGTTGTTGTTG	1375
QY	1261	AAGCATCAGAGACCCCAACTCTACAAGGCTTTCTTCTTCTCAGACCTGGCGAAATG	1320
DB	1376	AAGCATCAGAGACCCCAACTCTACAAGGCTTTCTTCTTCTCAGACCTGGCGAAATG	1435
QY	1321	TTAGCTGTGTTGCGGCTGGGAGGAGTCACTCATCTGTTAAAGTCCGTTGCTCGG	1380
DB	1436	TTAGCTGTGTTGCGGCTGGGAGGAGTCACTCATCTGTTAAAGTCCGTTGCTCGG	1495
QY	1381	GAATTTGGCCCAAGTCAAGGCTGTTGATGTTGATGTTGATGTTGTTGTTGTTG	1440
DB	1496	GAATTTGGCCCAAGTCAAGGCTGTTGATGTTGATGTTGATGTTGTTGTTGTTG	1555
QY	1441	CAGCCCTGGGTTCTCGGGAACCTCTGAGGAGTAAATTTTATTTTGGGAAGAAATACGA	1500
DB	1556	CAGCCCTGGGTTCTCGGGAACCTCTGAGGAGTAAATTTTATTTTGGGAAGAAATACGA	1615
QY	1501	AAGGAACGATATGAAAAAGTCTATAAGGCTTTGCTCTGAAAAAGGATTTACGCTGTTG	1560
DB	1616	AAGGAACGATATGAAAAAGTCTATAAGGCTTTGCTCTGAAAAAGGATTTACGCTGTTG	1675
QY	1561	GAGATGTTGATCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	1620
DB	1676	GAGATGTTGATCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	1735
QY	1621	GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACCAT	1680
DB	1736	GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACCAT	1795
QY	1681	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTATTTGTCAA	1740
DB	1796	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTATTTGTCAA	1855
QY	1741	ATTTTGCATGAGAGATCACAATTTTATGTTGATCTCATCATGTTGTCAGTACCTCAAGCTGA	1800
DB	1856	ATTTTGCATGAGAGATCACAATTTTATGTTGATCTCATCATGTTGTCAGTACCTCAAGCTGA	1915
QY	1801	AGTCAGATTTCTGATTTTGAAGATGTTAAATGTTGCAAGAGGGGACTTACACTGAGTTC	1860
DB	1916	AGTCAGATTTCTGATTTTGAAGATGTTAAATGTTGCAAGAGGGGACTTACACTGAGTTC	1975
QY	1861	CTAAAACTCTGTATAGATTTTGGGCTCCCTTTTAAAGAGGATAATAGGAAAGTGAACAA	1920
DB	1976	CTAAAACTCTGTATAGATTTTGGGCTCCCTTTTAAAGAGGATAATAGGAAAGTGAACAA	2035
QY	1921	CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG	1980
DB	2036	CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG	2095

Qy 1981 TCTCAACATCTTCTAGACCTCTTGAAGATGGTCTCTGGAGAGCCCAAGATACAGAG 2040  
 Db 2096 TCTCAACATCTTCTAGACCTCTTGAAGATGGTCTCTGGAGAGCCCAAGATACAGAG 2155  
 Qy 2041 AATGTCCAGTTACACTATCAGAGAGAACCGTTCTGAAGAGAAAGTTGGTTTTCAGGCC 2100  
 Db 2156 AATGTCCAGTTACACTATCAGAGAGAACCGTTCTGAAGAGAAAGTTGGTTTTCAGGCC 2215  
 Qy 2101 TATTAAGAAATTAATTCAGAGCTGGTGCTCACTGGATGTCCTTCAATTTTCTTATTCCTCTA 2160  
 Db 2216 TATTAAGAAATTAATTCAGAGCTGGTGCTCACTGGATGTCCTTCAATTTTCTTATTCCTCTA 2275  
 Qy 2161 AACACTCGAGCTCAGGTGCTATGCTGCTCAAGATTTGGTGGCTTCATCTCGGGCAAC 2220  
 Db 2276 AACACTCGAGCTCAGGTGCTATGCTGCTCAAGATTTGGTGGCTTCATCTCGGGCAAC 2335  
 Qy 2221 AAAACAAAGTATGCTAAATGTCACTGTAAATGGAGAGAGAAATGTAAACCGAAGCTAGAT 2280  
 Db 2336 AAAACAAAGTATGCTAAATGTCACTGTAAATGGAGAGAGAAATGTAAACCGAAGCTAGAT 2395  
 Qy 2281 CTTAACTGGTACTTAGGAATTTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGCATA 2340  
 Db 2396 CTTAACTGGTACTTAGGAATTTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGCATA 2455  
 Qy 2341 GCAAGATCTCTATTGGTATCTAGTCTCTGTTAACTCTTACAAACTTTGCAACAA 2400  
 Db 2456 GCAAGATCTCTATTGGTATCTAGTCTCTGTTAACTCTTACAAACTTTGCAACAA 2515  
 Qy 2401 ATGTTTGAAGTCAATCTGAAAGCTCCGGTATTTATTTGATAGAAATCCAAATAGGAAGA 2460  
 Db 2516 ATGTTTGAAGTCAATCTGAAAGCTCCGGTATTTATTTGATAGAAATCCAAATAGGAAGA 2575  
 Qy 2461 ATTTTAAATCGTTTCTCAAAAGACATTTGGAACACTTTGGATGATTTGCTCGCGTCAAGTTT 2520  
 Db 2576 ATTTTAAATCGTTTCTCAAAAGACATTTGGAACACTTTGGATGATTTGCTCGCGTCAAGTTT 2635  
 Qy 2521 TTAGATTTTCATCCAGACATTTGCTCAAGTGGTTGGTGGTCTCTGTTGGCTGTGCGCGTG 2580  
 Db 2636 TTAGATTTTCATCCAGACATTTGCTCAAGTGGTTGGTGGTCTCTGTTGGCTGTGCGCGTG 2695  
 Qy 2581 ATTCCTTTGGATCGCAATACCTCTGGTTCCCTCTGGAATCAATTTTCAATTTTCTTCGGCGA 2640  
 Db 2696 ATTCCTTTGGATCGCAATACCTCTGGTTCCCTCTGGAATCAATTTTCAATTTTCTTCGGCGA 2755  
 Qy 2641 TATTTTGGAAAAAGTCAAGAGATGTGAAGCGCTCGGAATCTCAAACTCGGAGTCCAGTG 2700  
 Db 2756 TATTTTGGAAAAAGTCAAGAGATGTGAAGCGCTCGGAATCTCAAACTCGGAGTCCAGTG 2815  
 Qy 2701 TTTTCCCACTTGTCTATCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760  
 Db 2816 TTTTCCCACTTGTCTATCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875  
 Qy 2761 GAGAGGTGTCAAGAACTGTTTGTATGTCACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2820  
 Db 2876 GAGAGGTGTCAAGAACTGTTTGTATGTCACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2935  
 Qy 2821 TTTTGTGACAAAGTCCCGTGGTTGCGCGTCTGCTGTGAGTCCATCTGTGCCATGTTTGTGTC 2880  
 Db 2936 TTTTGTGACAAAGTCCCGTGGTTGCGCGTCTGCTGTGAGTCCATCTGTGCCATGTTTGTGTC 2995  
 Qy 2881 ATCATCGTTGCTTGGGTCCCTGATTTCTGGCAAAACTCTGGATCCGGGCAGGTTGGT 2940  
 Db 2996 ATCATCGTTGCTTGGGTCCCTGATTTCTGGCAAAACTCTGGATCCGGGCAGGTTGGT 3055  
 Qy 2941 TTGGCACTGTCTATGCGCTCACGCTCATATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
 Db 3056 TTGGCACTGTCTATGCGCTCACGCTCATATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3115  
 Qy 3001 GCTGAAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATGGAATACAGACCTTGAA 3060  
 Db 3116 GCTGAAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATGGAATACAGACCTTGAA 3175

Qy 3061 AAAGAAGCACCTTGGGAATATCAGAAACGCCACACAGCCTGGCCCCCATGAAGGAGTG 3120  
 Db 3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCACACAGCCTGGCCCCCATGAAGGAGTG 3235  
 Qy 3121 ATAATCTTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3180  
 Db 3236 ATAATCTTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3295  
 Qy 3181 CTGACAGACTCATTAATCACAAGAAAAGTTGGCAATTTGGGAGAACCCGGAGCTGGA 3240  
 Db 3296 CTGACAGACTCATTAATCACAAGAAAAGTTGGCAATTTGGGAGAACCCGGAGCTGGA 3355  
 Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTGCAGAACCCGAAAGGTAAAAATTTGGATT 3300  
 Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTGCAGAACCCGAAAGGTAAAAATTTGGATT 3415  
 Qy 3301 GATAAGATCTTGAACAACCTGAAATTTGGAATTCACGATTTTAAAGGAAGAAAATGTCATCAT 3360  
 Db 3416 GATAAGATCTTGAACAACCTGAAATTTGGAATTCACGATTTTAAAGGAAGAAAATGTCATCAT 3475  
 Qy 3361 CCTCAGGAACTGTGTTTGTTCACCTGGGAACAATGAGGAAAACCTGGATCCCTTTTAATGAG 3420  
 Db 3476 CCTCAGGAACTGTGTTTGTTCACCTGGGAACAATGAGGAAAACCTGGATCCCTTTTAAGAG 3535  
 Qy 3421 CACACGATCAGGAACCTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCATTTGAA 3480  
 Db 3536 CACACGATCAGGAACCTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCATTTGAA 3595  
 Qy 3481 GATCTTCTGGTAAAAATGGAATACGAAATAGCAGAATCAGGATCCAAATTTTGTGTTGGA 3540  
 Db 3596 GATCTTCTGGTAAAAATGGAATACGAAATAGCAGAATCAGGATCCAAATTTTGTGTTGGA 3655  
 Qy 3541 CAAAGACAACTGTGTGCTTGCCTTGCAGGGCAATTTCTCAGGAAAATCAGATTTGATTTAT 3600  
 Db 3656 CAAAGACAACTGTGTGCTTGCCTTGCAGGGCAATTTCTCAGGAAAATCAGATTTGATTTAT 3715  
 Qy 3601 GATGAACGACGGCAAAATGTGGATCCCAAGAACTGATGAGTTTAAACAAAAAAATCCGG 3660  
 Db 3716 GATGAACGACGGCAAAATGTGGATCCCAAGAACTGATGAGTTTAAACAAAAAAATCCGG 3775  
 Qy 3661 GAGAAATTTGCCCATCTGACCCGTCTAACCAATTCGACACAGATTTGAAACACATTTATTGAC 3720  
 Db 3776 GAGAAATTTGCCCATCTGACCCGTCTAACCAATTCGACACAGATTTGAAACACATTTATTGAC 3835  
 Qy 3721 AGCGACAGATAATGTTTGTAGATTTCAGGAGACTGGAAGAAATATGATGAGCCGTATGTT 3780  
 Db 3836 AGCGACAGATAATGTTTGTAGATTTCAGGAGACTGGAAGAAATATGATGAGCCGTATGTT 3895  
 Qy 3781 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACCACTGGGCAAGGCAGAA 3840  
 Db 3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACCACTGGGCAAGGCAGAA 3955  
 Qy 3841 GCGCTGCCCTCACTGAAAAAGCAGAAAAACAGGTATATCTTCAAAAAGAAATTTATCCATATT 3900  
 Db 3956 GCGCTGCCCTCACTGAAAAAGCAGAAAAACAGGTATATCTTCAAAAAGAAATTTATCCATATT 4015  
 Qy 3901 GGTCACTGACCACTGTTTACAAACACTTCCAAATGGAAGCCCTCGACCTTAACTATT 3960  
 Db 4016 GGTCACTGACCACTGTTTACAAACACTTCCAAATGGAAGCCCTCGACCTTAACTATT 4075  
 Qy 3961 TTCGAGACAGCACTGTGA 3978  
 Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 12  
 ADB75177  
 ID ADB75177 standard; cDNA; 5870 BP.  
 XX  
 AC ADB75177;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX



Db 1496 GAATTTGGCCCCAAGTCACGGGCTGGTCAGCGTGATGGAAGATTGGCTATGTGTCACAG 1555  
Qy 1441 CAGCCCTGGGGTGTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1556 CAGCCCTGGGGTGTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615  
Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTTG 1560  
Db 1616 AAGGAACGATATGAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTTG 1675  
Qy 1561 GAGGATGGTATCTGATCTGATAGGAGATCGGGGAACCAAGCTGAGTGAGGGGACAGAAA 1620  
Db 1676 GAGGATGGTATCTGATCTGATAGGAGATCGGGGAACCAAGCTGAGTGAGGGGACAGAAA 1735  
Qy 1621 GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT 1680  
Db 1736 GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT 1795  
Qy 1681 CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
Db 1796 CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855  
Qy 1741 ATTTTGCATGAGAAGATCACAAATTTTAGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCA 1800  
Db 1856 ATTTTGCATGAGAAGATCACAAATTTTAGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCA 1915  
Qy 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAAATATGTTGTCAGAGGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATATTTGMAAGATGGTAAATATGTTGTCAGAGGGGACTTACACTGAGTTC 1975  
Qy 1861 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA 1920  
Db 1976 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGGTTTGG 1980  
Db 2036 CCTCCAGTTCCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGGTTTGG 2095  
Qy 1981 TCTCAACAAATCTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCCAAGATACAGAG 2040  
Db 2096 TCTCAACAAATCTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCCAAGATACAGAG 2155  
Qy 2041 AATGTCAGTTACACTATCAGAGAGAACCGTTTCTGAGGAAAAGTTGGTTTTCAGGCC 2100  
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Db 2216 TATAAGAAATTAATTCAGAGCTGGTGCTCAGTGGATTTGTTCTATTTTCTTATTTCTCTTA 2275  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTTATCTGGGCAAC 2220  
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Db 2396 CTTAACTGGTACTTAGGAAATTTATTTACAGTTTAACTGTAGCTACCGTTTCTTTTGGGATA 2455  
Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCCTGTTAACTCTTCAAACTTTGCAACAAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTAGCTCCTGTTAACTCTTCAAACTTTGCAACAAA 2515  
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Db 2516 ATGTTTGGTCAATTTCTGAAGCTCCGGTATTTATTTTGTAGTAATCCAAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCAAAAGACATTTGACACTTTGGATGATTTTGTGCGCGCTCACGTTT 2520

Db 2576 ATTTTAAATCGTTTCTCAAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTCACGTTT 2635  
Qy 2521 TTAGATTTTCATCCAGACATTTCTCAAGTGGTTGGTGTGTGTTCTCTGTGGCTGTGGCCGTG 2580  
Db 2636 TTAGATTTTCATCCAGACATTTCTCAAGTGGTTGGTGTGTGTTCTCTGTGGCTGTGGCCGTG 2695  
Qy 2581 ATTCCTTTGGATCGCAATACCTTGGTTCCCTCTGGAATCATTTTTCATTTTCTTTCTCGGGA 2640  
Db 2696 ATTCCTTTGGATCGCAATACCTTGGTTCCCTCTGGAATCATTTTTCATTTTCTTTCTCGGGA 2755  
Qy 2641 TATTTTGTGAAAACGTCACAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG 2700  
Db 2756 TATTTTGTGAAAACGTCACAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG 2815  
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Qy 2761 GAGAGGTGTGAGGAACGTGTGTGATGACACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2820  
Db 2876 GAGAGGTGTGAGGAACGTGTGTGATGACACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2935  
Qy 2821 TTTTGTGACAAACGTCCCGCTGCTGCGCGTCCGTCTGGATGCCATCTGTGCCATGTGTTGTC 2880  
Db 2936 TTTTGTGACAAACGTCCCGCTGCTGCGCGTCCGTCTGGATGCCATCTGTGCCATGTGTTGTC 2995  
Qy 2881 ATCATCGTTGGCTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCGGGCAGGTTGGT 2940  
Db 2996 ATCATCGTTGGCTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCGGGCAGGTTGGT 3055  
Qy 2941 TTGSCACTGTCTTATGCCCCACGCTCATGSGGATGTTTCAGTGGTGTGTTTCGCAAAAGT 3000  
Db 3056 TTGSCACTGTCTTATGCCCCACGCTCATGSGGATGTTTCAGTGGTGTGTTTCGCAAAAGT 3115  
Qy 3001 GCTGAACTTGGAGATATGATGATCTCAGTAGAAAAGGTTCATTTGAATACACAGACTTGAA 3060  
Db 3116 GCTGAACTTGGAGATATGATGATCTCAGTAGAAAAGGTTCATTTGAATACACAGACTTGAA 3175  
Qy 3061 AAAGAGCACTTTGGGAATATCAGAAACGCCACACACAGGCTGGCCCCCATGAAGGAGTG 3120  
Db 3176 AAAGAGCACTTTGGGAATATCAGAAACGCCACACACAGGCTGGCCCCCATGAAGGAGTG 3235  
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Db 3296 CTGACGACCTCATTTAAATCAAAAGAAAAGTTGGCAATTTGGGAAGAAACCGGAGCTGGA 3355  
Qy 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTAGATTGTTCAGAACCGGAAGGTAAAATTTGGATT 3300  
Db 3356 AAAAGTTCCCTCATCTCAGGCCCTTTTAGATTGTTCAGAACCGGAAGGTAAAATTTGGATT 3415  
Qy 3301 GATAAGATCTTGACAACTGAAAATTTGGAATTCACGATTTAAGGAAGAAAATCTCAATCAT 3360  
Db 3416 GATAAGATCTTGACAACTGAAAATTTGGAATTCACGATTTAAGGAAGAAAATCTCAATCAT 3475  
Qy 3361 CCTCAGGAACCTGTGTTTGTTCACCTGGAAACATAGAGGAAAAACCTGGATCCCTTTAATGAG 3420  
Db 3476 CCTCAGGAACCTGTGTTTGTTCACCTGGAAACATAGAGGAAAAACCTGGATCCCTTTAAGGAG 3535  
Qy 3421 CACACGATGAGGAACGTGTGGAAATGCCCTTACAGAGGTACAACTTAAAGAAACCATTCGA 3480  
Db 3536 CACACGATGAGGAACGTGTGGAAATGCCCTTACAGAGGTACAACTTAAAGAAACCATTCGA 3595  
Qy 3481 GATCTTCTGTGTAATAATGGATGAAATAGCAGAAATCAGGATCCAAATTTTAGTGTTCGA 3540  
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Qy 3541 CAAAGACAACTGGTGTGCTGCTGCGAGGCAATTTCTCAGGAAAAATCAGATATTGATTTAT 3600  
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Qy	3601	GATGAAGCGACGGCAAAATGTGGATCCAAAGAACTGATGAGTTAAATACAAAAAATAATCCGG	3660
Db	3716	GATGAAGCGACGGCAAAATGTGGATCCAAAGAACTGATGAGTTAAATACAAAAAATAATCCGG	3775
Qy	3661	GAGAAATTTGCCCACTGCACCGTGCTAACCAATTCACACAGATTGAAACACCATTAATTGAC	3720
Db	3776	GAGAAATTTGCCCACTGCACCGTGCTAACCAATTCACACAGATTGAAACACCATTAATTGAC	3835
Qy	3721	AGCACAAGATAATGGTTTTAGATTCAAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT	3780
Db	3836	AGCACAAGATAATGGTTTTAGATTCAAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT	3895
Qy	3781	TTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGGCAAGCGCAGAA	3840
Db	3896	TTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGGCAAGCGCAGAA	3955
Qy	3841	GCCGCTGCCCTCACTGAACACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT	3900
Db	3956	GCCGCTGCCCTCACTGAACACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT	4015
Qy	3901	GGTCACACTGACCAATGGTTTACAAACACTTTCCAAATGGACAGCCCTCGACCTTAACTATT	3960
Db	4016	GGTCACACTGACCAATGGTTTACAAACACTTTCCAAATGGACAGCCCTCGACCTTAACTATT	4075
Qy	3961	TTTGAGACAGCACTGTGA	3978
Db	4076	TTTGAGACAGCACTGTGA	4093

## RESULT 13

ABV75072

ID ABV75072 standard: DNA: 4231 BP.

XX

AC ABV75072;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human DevG4 homologue protein encoding DNA.

XX.

KW Protein disulfide isomerase; DevG20; ABC transporter; DevG4; DevG22;  
 KW anorectic; immunomodulator; antidepressant; antidiabetic; hypotensive;  
 KW antiarteriosclerotic; antileptic; osteopathic; antiarthritic; gene;  
 KW litholytic; hepatotropic; cytostatic; neuroprotective; gene therapy;  
 KW transgenic; human; ds.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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100	0.0000	0.0000

FT /\*tag= a

FT /product= "DevG4 homologue protein"

XX

PN WO200279238-A2.

XX

PD 10-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-EP003540.

XX

PR 02-APR-2001; 2001EP-00108315.

PR 01-0

XX

PA (DE)

XX

PI Eul.

XX

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100	100

DR P-PSDB; ABB82645.

XX

PT New protein disul

PT pol.

PT hypertension, heart disease, hypercholesterolemia, osteoarthritis,  
PT gallstones or cancer.

Db 716 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGTGGCGAGCACCACTG 775  
Qy 661 CAGCGATCGCAGTACCTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 720  
Db 776 CAGCGATCGCAGTACCTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835  
Qy 721 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 780  
Db 836 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 895  
Qy 781 CTGAGGAGTAAACTGCAACTTTTCAACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAACTGCAACTTTTCAACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955  
Qy 841 ACTGGTATAGGATAATAAAGATGTACGCTGGGAAAAGTCATTTTCAAAATCTTATTACC 900  
Db 956 ACTGGTATAGGATAATAAAGATGTACGCTGGGAAAAGTCATTTTCAAAATCTTATTACC 1015  
Qy 901 AATTGTGAAGAAGAGAGATTTTCAAGATTTCTGAAGAAGTTCTTGCCCTCAGGGGATGAAT 960  
Db 1016 AATTGTGAAGAAGAGAGATTTTCAAGATTTCTGAAGAAGTTCTTGCCCTCAGGGGATGAAT 1075  
Qy 961 TTGGCTTTCGTTTTTTCAGTGCAGCAAAATCATCGTGTGTGTGACCTTCAACCCTACGTG 1020  
Db 1076 TTGGCTTTCGTTTTTTCAGTGCAGCAAAATCATCGTGTGTGTGACCTTCAACCCTACGTG 1135  
Qy 1021 CTCTCGCGAGTGTGATCAGCCAGCCGCGTGTTCGTGGCAGTGCAGCTGTATGGGGCT 1080  
Db 1136 CTCTCGCGAGTGTGATCAGCCAGCCGCGTGTTCGTGGCAGTGCAGCTGTATGGGGCT 1195  
Qy 1081 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1140  
Db 1196 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1255  
Qy 1141 GTCAGCATCCGAAGAATCCAGACCTTTTGTACTTGTATGAGATATCAGAGCGCAACCGT 1200  
Db 1256 GTCAGCATCCGAAGAATCCAGACCTTTTGTACTTGTATGAGATATCAGAGCGCAACCGT 1315  
Qy 1201 CAGCTGCCGTGAGTGTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1260  
Db 1316 CAGCTGCCGTGAGTGTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1375  
Qy 1261 AAGGCATCAGAGACCCCACTCTACAAGCCCTTTCCTTACTGTGCAGACCTGGCGAATTG 1320  
Db 1376 AAGGCATCAGAGACCCCACTCTACAAGCCCTTTCCTTACTGTGCAGACCTGGCGAATTG 1435  
Qy 1321 TTAGCTGTGTCGGCCCGTGGGAGCAGGGAAGTCATCACTGTTTAAAGTCGGTCTCGGG 1380  
Db 1436 TTAGCTGTGTCGGCCCGTGGGAGCAGGGAAGTCATCACTGTTTAAAGTCGGTCTCGGG 1495  
Qy 1381 GAATTGGCCCCAAGTCAAGGCTGGTGCAGGTGCATCGNAGAAATTCCTATGTGCTCAG 1440  
Db 1496 GAATTGGCCCCAAGTCAAGGCTGGTGCAGGTGCATCGNAGAAATTCCTATGTGCTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAAGAAATAGAA 1615  
Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTG 1560  
Db 1616 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTG 1675  
Qy 1561 GAGGATGGTGNATCTGACTGTGATAGGAGATCGGGGAACCGCTGAGTGGAGGCGAGAAA 1620  
Db 1676 GAGGATGGTGNATCTGACTGTGATAGGAGATCGGGGAACCGCTGAGTGGAGGCGAGAAA 1735  
Qy 1621 GCAGGCTGTAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT 1680  
Db 1736 GCAGGCTGTAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT 1795  
Qy 1681 CCTCTCAGTGCAGTGTAGTGCAGAAAGTTAGCAGACACTTGTGTCGAACCTGTGTATTGTCAA 1740  
Db 1796 CCTCTCAGTGCAGTGTAGTGCAGAAAGTTAGCAGACACTTGTGTCGAACCTGTGTATTGTCAA 1855

Qy 1741 ATTTTGATCAGGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1800  
Db 1856 ATTTTGATCAGGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915  
Qy 1801 AGTCAGATTTCTGATPATTTGAAAGATGTTAAATGTTGTCAGAAAGGGACCTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATPATTTGAAAGATGTTAAATGTTGTCAGAAAGGGACCTTACACTGAGTTC 1975  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGGAAGTGAACAA 1920  
Db 1976 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGGAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCACAGAACTCCACACTAAGGAATCGTACTTCTCAGAGTCTTTCGGTTTGG 1980  
Db 2036 CCTCCAGTTCACAGAACTCCACACTAAGGAATCGTACTTCTCAGAGTCTTTCGGTTTGG 2095  
Qy 1981 TCTCAACAATCTTCTAGACCTCTCTTGAAAGATGGTGTCTCTGGAGAGCCCAAGATACAGAG 2040  
Db 2096 TCTCAACAATCTTCTAGACCTCTCTTGAAAGATGGTGTCTCTGGAGAGCCCAAGATACAGAG 2155  
Qy 2041 AATGTCCAGTTTACACTATCAGAGGAAACCGTTCTGAAGAAAAGTTGGTTTTCAGGCC 2100  
Db 2156 AATGTCCAGTTTACACTATCAGAGGAAACCGTTCTGAAGAAAAGTTGGTTTTCAGGCC 2215  
Qy 2101 TATAAGAAATTTACTTTTACAGAGCTGGTGTCTCACTGGATTTCTTTCATTTTCTTATTTCTCTA 2160  
Db 2216 TATAAGAAATTTACTTTTACAGAGCTGGTGTCTCACTGGATTTCTTTCATTTTCTTATTTCTCTA 2275  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTCTTTCAAGATTTGGTGGCTTTTCATACTGGGCAAAAC 2220  
Db 2276 AACACTGCAGCTCAGGTTGCTATGTCTTTCAAGATTTGGTGGCTTTTCATACTGGGCAAAAC 2335  
Qy 2221 AACAAAGTATGCTAAATGTCTGTAATGAGGAGGAGAAATGTAAACGAGAACTAGAT 2280  
Db 2336 AACAAAGTATGCTAAATGTCTGTAATGAGGAGGAGAAATGTAAACGAGAACTAGAT 2395  
Qy 2281 CTTAACTGGTACTTTAGGAAATTTTACAGTGTAACTGTAGCTACCGTCTCTTTTGGGATA 2340  
Db 2396 CTTAACTGGTACTTTAGGAAATTTTACAGTGTAACTGTAGCTACCGTCTCTTTTGGGATA 2455  
Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCTTTTAACTCTTTCACAAAATTTGCAACAACAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTAGCTCTTTTAACTCTTTCACAAAATTTGCAACAACAA 2515  
Qy 2401 ATGTTTGAGTCAATTTGAAAGCTCCCGTATTTTCTTGTATAGAAATCCAATAGGAGA 2460  
Db 2516 ATGTTTGAGTCAATTTGAAAGCTCCCGTATTTTCTTGTATAGAAATCCAATAGGAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACATTTGGATGATTTTGTCTGCCCTGACCGTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACATTTGGATGATTTTGTCTGCCCTGACCGTTT 2635  
Qy 2521 TTAGATTTTCAATCCAGACATTTGCTACAAAGTGGTGTGGTGTCTCTGTGGCTGTGGCCGTG 2580  
Db 2636 TTAGATTTTCAATCCAGACATTTGCTACAAAGTGGTGTGGTGTCTCTGTGGCTGTGGCCGTG 2695  
Qy 2581 ATTCCTTGGATCGCAATACCTTGGTTCCCTTGGAAATCATTTTTCATTTTCTTGGCGA 2640  
Db 2696 ATTCCTTGGATCGCAATACCTTGGTTCCCTTGGAAATCATTTTTCATTTTCTTGGCGA 2755  
Qy 2641 TATTTTGGAAACGTCACAGAGATGTGAAGCCCTGGAAATCTACAACTCGGAGTCCAAGT 2700  
Db 2756 TATTTTGGAAACGTCACAGAGATGTGAAGCCCTGGAAATCTACAACTCGGAGTCCAAGT 2815  
Qy 2701 TTTTCCCACTTGTCTATCTCTCCAGGGCTCTGGACCAATCCGGGCAATACAAAGCAAA 2760  
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Db 2876 GAGAGGTGTGAGGAACTGTTTGTATGACACAGGATTTTACATTCAGAGGCTTGGTCTTGT 2935

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QY 2821 TTTTGGACAGCTCCCGTGGTTCGCGCTCGTCTGAGTGCATCTGTGCCATGTTTGTG 2880
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QY 2881 ATCATCGTTGCTTTGGTCCCTGATTTCTGCAAAAACCTCTGGATCGCGGACGTTGGT 2940
Db 2996 ATCATCGTTGCTTTGGTCCCTGATTTCTGCAAAAACCTCTGGATCGCGGACGTTGGT 3055
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QY 3001 GCTGAAGTTGAGAAATATGATCTCAGTAGAAAAGGTCAATTGAATACACAGACCTTGAA 3060
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QY 3061 AAGAAGCACCCTTGGGAATATCAGAAACCCACACAGCCTGCGCCCATGAAGGAGTG 3120
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QY 3121 ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGTGTACTGAAGCAT 3180
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QY 3181 CTGACAGCACTCATTAATACAGAAAGAAAGTTGGCAATTTGGGAAGAACCGGAGCTTGA 3240
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QY 3241 AAAAGTTCCCTCATCTCAGCCCTTTTAGATTTGTTCAGAACCCGAGGTAAATTTGGATT 3300
Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTAGATTTGTTCAGAACCCGAGGTAAATTTGGATT 3415
QY 3301 GATAAGATCTTGACAACTGAAATTTGAGCTTCAAGATTTAAGGAAGAAATGTCAATCATA 3360
Db 3416 GATAAGATCTTGACAACTGAAATTTGAGCTTCAAGATTTAAGGAAGAAATGTCAATCATA 3475
QY 3361 CCTCAGGAACCTGTTTGTTCACCTGGAACCAATGAGGAAAAACCTGGATCCCTTTAATGAG 3420
Db 3476 CCTCAGGAACCTGTTTGTTCACCTGGAACCAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535
QY 3421 CACACGATGAGGAACTGTGGATGCTTACAGAGGTACAACTTAAGAAACCATTTGAA 3480
Db 3536 CACACGATGAGGAACTGTGGATGCTTACAGAGGTACAACTTAAGAAACCATTTGAA 3595
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Db 3596 GATCTTCTCGTAAATAGGATCTGAATTAGCAGATCAGATCCAATTTTAGTGTGGA 3655
QY 3541 CAAAGACAACTGGTGTGCTTGGCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT 3600
Db 3656 CAAAGACAACTGGTGTGCTTGGCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT 3715
QY 3601 GATGAAGCAGCGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAAAATCCGG 3660
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QY 3661 GAGAAATTTCCCACTGACCGTGTCAACCAATTTGACACAGATTTGAACCAATTTATTGAC 3720
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Db 3896 TTGCTGCAAAATAAGAGACCTATTTTACAGATGTGTGCAACAACTGGGCAAGGCGAGAA 3955
QY 3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATCTTTCAAAAGAAATTTACACATATT 3900
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QY 3901 GGTCACTGACCACTGGTTTACAAACACATTTCCAATGGACAGCCCTCGACCTTAACTATT 3960
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Db 4016 GGTCACTGACCATGCTGGTTACAAACACTTCCAAATGGACAGCCCTGCACCTTAACATT 4075
QY 3961 TTCGAGACAGCACTGTGA 3978
Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 14
AAH93828
ID AAH93828 standard; cDNA; 6082 BP.
XX
AC AAH93828;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific 1st full length cDNA sequence for P510S.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN W0200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI Wang A, Mesgher WJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
PS Claim 1; Page 411-412; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAH0115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 U; 0 Other;
Query Match 99.7%; Score 3966; DB 4; Length 6082;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGCTGCCCTGTGTTACAGGAGGTGAAGCCCAACCCGCTGAGGACGCGAACTCTGTCTCA 60
Db 186 ATGCTGCCCTGTGTTACAGGAGGTGAAGCCCAACCCGCTGAGGACGCGAACTCTGTCTCA 245
QY 61 CGCGTGTCTTCTTGTGGTGGCTCAATCCCTTGTAAATTTGGCCATAAACCGAGATTAGAG 120
Db 246 CGCGTGTCTTCTTGTGGTGGCTCAATCCCTTGTAAATTTGGCCATAAACCGAGATTAGAG 305
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QY 121 GAAGATGATGTTATTCAGTCTGCCAGAGACCGCTCAGACACCTTGGAGGAGTTG 180  
DB 306 GAAGATGATGTTATTCAGTCTGCCAGAGACCGCTCAGACACCTTGGAGGAGTTG 365  
QY 181 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAAAGCCTTCTTTA 240  
DB 366 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAAAGCCTTCTTTA 425  
QY 241 ACAAGACAATCAPAAAGTGTTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
DB 426 ACAAGACAATCAPAAAGTGTTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 485  
QY 301 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 360  
DB 486 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 545  
QY 361 GAAATTTATGATCCCATGGATTCGTGGCTTTGAAACACAGCGTACGCTATGCCACGGTG 420  
DB 546 GAAATTTATGATCCCATGGATTCGTGGCTTTGAAACACAGCGTACGCTATGCCACGGTG 605  
QY 421 CTGACTTTTTCACGCTCATTTTGGCTATATCTGCAATCACTTATATTTTATFCAGTTTCAG 480  
DB 606 CTGACTTTTTCACGCTCATTTTGGCTATATCTGCAATCACTTATATTTTATFCAGTTTCAG 665  
QY 481 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATCTCGT 540  
DB 666 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATCTCGT 725  
QY 541 CTTAGTAACATGGCCATGGGGAAGACAACACACAGCCAGATAGTCAATCTGCTGTCCAAT 600  
DB 726 CTTAGTAACATGGCCATGGGGAAGACAACACACAGCCAGATAGTCAATCTGCTGTCCAAT 785  
QY 601 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACCTG 660  
DB 786 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACCTG 845  
QY 661 CAGCGATCGCAGTACCTGCTACTCTGGATGAGATAGGAATATCGTGCCTTGTCTGGG 720  
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PR 09-NOV-2000; 2000US-00709729.  
XX (CORI-) CORIXA CORP.  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
XX WPI; 2001-639232/73.  
DR P-PSDB; AAU69823.  
XX New human prostate-specific polypeptides and polynucleotides useful for  
PT the diagnosis and treatment of cancer, especially prostate cancer.  
XX Claim 1; Page 410-412; 579pp; English.  
XX The invention relates to isolated prostate-specific polynucleotides,  
CC polypeptides, fusion proteins of the polypeptides, antibodies raised  
CC against the polypeptides (or antigenic epitopes derived from them) and  
CC antigen-presenting cells expressing the polypeptides. The antibodies are  
CC useful for detecting the presence of cancer, especially prostate cancer.  
CC The polypeptides, polynucleotides and the antigen-presenting cells are  
CC useful for stimulating and/or expanding T cells specific for a tumour  
CC protein, and for inhibiting the development of cancer especially prostate  
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are  
CC useful for stimulating an immune response, and for treating cancer. The  
CC oligonucleotide is useful for detecting cancer. The present sequence is a  
CC prostate specific polynucleotide of the invention  
XX  
SQ Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 U; 0 Other;  
  
Query March 99.7%; Score 3966; DB 4; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
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Db 186 ATGCTGCCGTGTAACAGGAGTCAAGCCCAACCGCTGCAGGACGGCACTCTGCTCA 245  
  
Qy 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTAAAAATTTGGCCATAAACGGAGATTAG 120  
Db 246 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTAAAAATTTGGCCATAAACGGAGATTAG 305  
  
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Qy 181 CAAGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGAACCTTCTTTTA 240  
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Qy 301 ATTGAGGAAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 360  
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Qy 361 GAAATATATGATCCCATGATTCGTGGCTTTTGAACACAGCGTACGCCATATGCCACGGTG 420  
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Qy 421 CTGACTTTTTGACGCTCATTTTGGCTACTGTCATCACTTATATTTTATACGTTTCAG 480  
Db 606 CTGACTTTTTGACGCTCATTTTGGCTACTGTCATCACTTATATTTTATACGTTTCAG 665  
  
Qy 481 TGTCTGGGATCAGTTACGAGTAGCCATGTCATATGATTTATCGGAAGGCATTCGT 540  
Db 666 TGTCTGGGATCAGTTACGAGTAGCCATGTCATATGATTTATCGGAAGGCATTCGT 725  
  
Qy 541 CTTAGTAAACATGGGCATGGGGAAGACACACACAGCCAGATAGTCAATCTCTGCTCCAAT 600  
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Db 726 CTTAGTAAACATGGCCATGGGGAAGACAAACACAGCCAGATAGTCAATCTGCTGTCCAAT 785  
Qy 601 GATGTGAACAAGTTTGNATCAGGTGACAGTGTCTTACACTTCTGTTGGGAGGACCACTG 660  
Db 786 GATGTGAACAAGTTTGNATCAGGTGACAGTGTCTTACACTTCTGTTGGGAGGACCACTG 845  
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Qy 721 ATGCGAGTTCTAATCAFTTCTCTGCCCTTCCAAAGCTGTTTGGGAAGTGTCTCTCAATCA 780  
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Search completed: May 20, 2005, 04:30:37  
Job time : 1997 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2005, 03:46:56 ; Search time 2476 Seconds  
(without alignments)

9852.332 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcgcgtgtaccagga.....ttttcagagacgactgtga 3978

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	3973.2	99.9	4231	10	US-09-930-213-287
3	3973.2	99.9	4231	17	US-10-295-027-571
4	3973.2	99.9	4231	19	US-10-889-503-1
5	3973.2	99.9	5870	15	US-10-205-823-1
6	3973.2	99.9	5871	19	US-10-887-553A-717
7	3966	99.7	6082	9	US-09-759-143-535
8	3966	99.7	6082	9	US-09-780-669-535
9	3966	99.7	6082	9	US-09-822-827-535
10	3966	99.7	6082	9	US-09-895-793-535
11	3966	99.7	6082	9	US-09-895-814-535

Sequence 535, App  
Sequence 535, App  
Sequence 535, App  
Sequence 535, App  
Sequence 20660, A  
Sequence 24403, A  
Sequence 24177, A  
Sequence 24569, A  
Sequence 26500, A  
Sequence 28237, A  
Sequence 50, Appl  
Sequence 59, Appl  
Sequence 536, App  
Sequence 536, App  
Sequence 536, App  
Sequence 536, App  
Sequence 536, App  
Sequence 1007, App  
Sequence 1007, App  
Sequence 1006, App  
Sequence 1006, App  
Sequence 1006, App  
Sequence 56, Appl  
Sequence 613, App  
Sequence 824, App  
Sequence 824, App  
Sequence 824, App  
Sequence 824, App

#### ALIGNMENTS

#### RESULT 1

US-10-295-027-569

Sequence 569, Application US/10295027

Publication No. US20030232350A1

GENERAL INFORMATION:

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APPLICANT: Murray, Richard

APPLICANT: Watson, Susan R.

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

FILE REFERENCE: 018501-012500US

CURRENT APPLICATION NUMBER: US/10/295,027

PRIOR FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US 09/663,733

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PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/335,394

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PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR FILING DATE: 2002-01-08

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; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 569
; LENGTH: 3978
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-569

Query Match      100.0%; Score 3978; DB 17; Length 3978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCCGTGTACCAAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60
Db 1 ATGCTGCCGTGTACCAAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60

Qy 61 CGCGTGTCTTCTGCTGCTCAATCCCTTGTTTAAATTTGCCATAAACGGAGATTAGAG 120
Db 61 CGCGTGTCTTCTGCTGCTCAATCCCTTGTTTAAATTTGCCATAAACGGAGATTAGAG 120

Qy 121 GAAGATGATATGATTTCAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180
Db 121 GAAGATGATATGATTTCAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180

Qy 181 CAAGGGTTCGGGATAAAGAAAGTTTAAAGAGTGAAGATGACGACAGAGCCCTCTTTA 240
Db 181 CAAGGGTTCGGGATAAAGAAAGTTTAAAGAGTGAAGATGACGACAGAGCCCTCTTTA 240

Qy 241 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTGA 300
Db 241 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTGA 300

Qy 301 ATTGAGAAAGTGCCAAAGTAATCCAGCCCAATTTTTGGGAAATTTATTAATTTT 360
Db 301 ATTGAGAAAGTGCCAAAGTAATCCAGCCCAATTTTTGGGAAATTTATTAATTTT 360

Qy 361 GAAATTTATGATCCCATGGATTCTGGCTTATCTGCACTCATATATTTTATCAGTTTCA 420
Db 361 GAAATTTATGATCCCATGGATTCTGGCTTATCTGCACTCATATATTTTATCAGTTTCA 420

Qy 421 CTGACTTTTTGACGCTCAATTTGGCTATCTGCACTCATATATTTTATCAGTTTCA 480
Db 421 CTGACTTTTTGACGCTCAATTTGGCTATCTGCACTCATATATTTTATCAGTTTCA 480

Qy 481 TGTCTGGGATGAGGTTACGAGTACGATAGTCCATATGATTTATCGGAAGGCACTTCGT 540
Db 481 TGTCTGGGATGAGGTTACGAGTACGATAGTCCATATGATTTATCGGAAGGCACTTCGT 540

Qy 541 CTTAGTAAATGAGGTTTGAATCAGTGTGATGATGATGATGATGATGATGATGATGAT 600
Db 541 CTTAGTAAATGAGGTTTGAATCAGTGTGATGATGATGATGATGATGATGATGATGAT 600

Qy 601 GATGTGAACAAAGTTTGAATCAGTGTGATGATGATGATGATGATGATGATGATGATG 660
Db 601 GATGTGAACAAAGTTTGAATCAGTGTGATGATGATGATGATGATGATGATGATGATG 660

Qy 661 CAGCGATGCGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 CAGCGATGCGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

Qy 721 ATGCGAGTCTTAATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ATGCGAGTCTTAATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

Qy 781 CTGAGGAGTAAACATGCACTTTTCAAGATGCGAGGATCAGGACCATGAATGAAGTTATA 840
Db 781 CTGAGGAGTAAACATGCACTTTTCAAGATGCGAGGATCAGGACCATGAATGAAGTTATA 840
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781 CTGAGGAGTAAACATGCACTTTTCAAGATGCGAGGATCAGGACCATGAATGAAGTTATA 840
841 ACTGGTATAAGGATAATAAATAATGACGCTGGGAAAAGTCAATTTTCAAAATCTTATTACC 900
841 ACTGGTATAAGGATAATAAATAATGACGCTGGGAAAAGTCAATTTTCAAAATCTTATTACC 900
901 AATTGGAAGAAGAGAGATTTCAGAGATTCTCAGAAAGTTCTCGCTCAGGGGATCAAT 960
901 AATTGGAAGAAGAGAGATTTCAGAGATTCTCAGAAAGTTCTCGCTCAGGGGATCAAT 960
961 TTGGCTTCGTTTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCAACACCTACGTG 1020
961 TTGGCTTCGTTTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCAACACCTACGTG 1020
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1081 GTGGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1140
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1141 GTCAGCATCCGAAGAATCCAGACCTTTTCTACTTCTGATGAGATATCACAGCGCAACCGT 1200
1201 CAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
1201 CAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
1261 AAGGCATCAGACACCCCACTCTACAGGCTTTTCTTACTGTCAGACCTTGGGCAATTTG 1320
1261 AAGGCATCAGACACCCCACTCTACAGGCTTTTCTTACTGTCAGACCTTGGGCAATTTG 1320
1321 TTAGCTGTGCTGGGCTGGGAGAGTCACTCACTGTTAACTGCGCTGCTCGGG 1380
1321 TTAGCTGTGCTGGGCTGGGAGAGTCACTCACTGTTAACTGCGCTGCTCGGG 1380
1381 GAATTTGCCCAAGTCAAGGCTGGTCAAGTGTGATGGAAGATTTGCTATGCTCTCAG 1440
1381 GAATTTGCCCAAGTCAAGGCTGGTCAAGTGTGATGGAAGATTTGCTATGCTCTCAG 1440
1441 CAGCCCTGGGCTTCTCGGAACTCTGAGGAGTAAATTTTATTTGGGAAAGATAGCAA 1500
1441 CAGCCCTGGGCTTCTCGGAACTCTGAGGAGTAAATTTTATTTGGGAAAGATAGCAA 1500
1501 AAGGAAAGTATGAAAGTCTGCTCTGAAAGGATTTTACAGCTGTG 1560
1501 AAGGAAAGTATGAAAGTCTGCTCTGAAAGGATTTTACAGCTGTG 1560
1561 GAGGATGGTCTGCTGATGAGGATCGGGGAAACCGCTGAGTGGAGGGCAGAA 1620
1561 GAGGATGGTCTGCTGATGAGGATCGGGGAAACCGCTGAGTGGAGGGCAGAA 1620
1621 GCAGGCTAAACCTTCAAGAGCAGTGTATCAAGATCTGACATCTATCTCTGGAAGAT 1680
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1681 CCTCTCAGTGCAGTGTGAGGAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740
1681 CCTCTCAGTGCAGTGTGAGGAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740
1741 ATTTTGCATGAGAGATCAAAATTTTGTGATCTCATCAGTGTGAGTACCTCAAGAGCTGCA 1800
1741 ATTTTGCATGAGAGATCAAAATTTTGTGATCTCATCAGTGTGAGTACCTCAAGAGCTGCA 1800
1801 AGTCAGATCTGATATTTGAAAGATGTAATGTCGAGAGGGGACTTACACTGAGTTTC 1860
1801 AGTCAGATCTGATATTTGAAAGATGTAATGTCGAGAGGGGACTTACACTGAGTTTC 1860
1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 1920
1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 1920
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Qy	1921	CCTCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG	1980
Db	1921	CCTCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG	1980
Qy	1981	TCTCAACAATCTTCTAGACCTCTTGAAGATGGTGTCTCGAGAGCCAAAGATACAGAG	2040
Db	1981	TCTCAACAATCTTCTAGACCTCTTGAAGATGGTGTCTCGAGAGCCAAAGATACAGAG	2040
Qy	2041	AATGTCAGTACACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC	2100
Db	2041	AATGTCAGTACACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC	2100
Qy	2101	TATAAGAAATTAATTCAGAGCTGGTGCTCACTGGATTTGTTCTTCAATTTCTCCTA	2160
Db	2101	TATAAGAAATTAATTCAGAGCTGGTGCTCACTGGATTTGTTCTTCAATTTCTCCTA	2160
Qy	2161	AACACTGAGCTCAGGTTCCTATGTGCTTCAAGATTGGTGGCTTTCATCTGGGCAAC	2220
Db	2161	AACACTGAGCTCAGGTTCCTATGTGCTTCAAGATTGGTGGCTTTCATCTGGGCAAC	2220
Qy	2221	AAACAAAGTATGCTAAATGTCACTGTAATCGAGGAGGAATGTAAACCGAGAAGCTAGAT	2280
Db	2221	AAACAAAGTATGCTAAATGTCACTGTAATCGAGGAGGAATGTAAACCGAGAAGCTAGAT	2280
Qy	2281	CTTAACCTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Db	2281	CTTAACCTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Qy	2341	GCAAGATCTCTATTTGGTATTCTAGCTCTTGTAACTCTTCAAAAATTTGCAACAA	2400
Db	2341	GCAAGATCTCTATTTGGTATTCTAGCTCTTGTAACTCTTCAAAAATTTGCAACAA	2400
Qy	2401	ATGTTTGGATCAATCTGGAAGCTCCGGTATTTCTTTGATAGAAATCCAATAGGAGA	2460
Db	2401	ATGTTTGGATCAATCTGGAAGCTCCGGTATTTCTTTGATAGAAATCCAATAGGAGA	2460
Qy	2461	ATTTTAAATCGTTTCTCAAAAGACATTTGGAACATTTGGATGATTTGCTGCGCTGACGTTT	2520
Db	2461	ATTTTAAATCGTTTCTCAAAAGACATTTGGAACATTTGGATGATTTGCTGCGCTGACGTTT	2520
Qy	2521	TTAGATTTTCAGACAGATTTGCTAAGATGGTGGTGGTCTCTGTGGCTGTGGCGGTG	2580
Db	2521	TTAGATTTTCAGACAGATTTGCTAAGATGGTGGTGGTCTCTGTGGCTGTGGCGGTG	2580
Qy	2581	ATTCCTTTGGATCGCAATACCTGTTCCCTCGGAATCAATTTTCAATTTTCTTGGCGA	2640
Db	2581	ATTCCTTTGGATCGCAATACCTGTTCCCTCGGAATCAATTTTCAATTTTCTTGGCGA	2640
Qy	2641	TATTTTGGAAACGTCAGAGATGTGAAGCGCTTGAATCTACAACTCGGAGTCCAGTG	2700
Db	2641	TATTTTGGAAACGTCAGAGATGTGAAGCGCTTGAATCTACAACTCGGAGTCCAGTG	2700
Qy	2701	TTTTCCCACTTGTCATCTTCTCTCAGGGGCTTGGACCATTCGGGCAATAAAAGCAGAA	2760
Db	2701	TTTTCCCACTTGTCATCTTCTCTCAGGGGCTTGGACCATTCGGGCAATAAAAGCAGAA	2760
Qy	2761	GAGAGGTGTGAGGAACCTTTGATGCAACACAGGATTTACATTCAGAGGCTTGGTTCTTG	2820
Db	2761	GAGAGGTGTGAGGAACCTTTGATGCAACACAGGATTTACATTCAGAGGCTTGGTTCTTG	2820
Qy	2821	TTTTTGAACAACGTCCTGCTGGTCTCGCTCTGGATGCCATCTGTGCCATGTTTGTGTC	2880
Db	2821	TTTTTGAACAACGTCCTGCTGGTCTCGCTCTGGATGCCATCTGTGCCATGTTTGTGTC	2880
Qy	2881	ATCATCTGTTGGTTCCTGCTGATTTCTGGCAAAAACCTCTGGATCGCGGCAAGTTGGT	2940
Db	2881	ATCATCTGTTGGTTCCTGCTGATTTCTGGCAAAAACCTCTGGATCGCGGCAAGTTGGT	2940
Qy	2941	TTGSCACTGTCTATGCTCCTCACGCTCATGCGGATGTTTCACTGGTGTGTTTCGACAAAGT	3000
Db	2941	TTGSCACTGTCTATGCTCCTCACGCTCATGCGGATGTTTCACTGGTGTGTTTCGACAAAGT	3000

Qy	3001	GCTGAAGTTGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA	3060
Db	3001	GCTGAAGTTGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA	3060
Qy	3061	AAAGAAGCACTTGGGAATATCAGAAAGCCCAACACAGCCTGGCCCCCATGAAGAGTG	3120
Db	3061	AAAGAAGCACTTGGGAATATCAGAAAGCCCAACACAGCCTGGCCCCCATGAAGAGTG	3120
Qy	3121	ATAATCTTTGCAATATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGCTACTGAAGCAT	3180
Db	3121	ATAATCTTTGCAATATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGCTACTGAAGCAT	3180
Qy	3181	CTGACAGCACTCATTTAAATCAAGAAGAGTTGGCATTTGTGGGAAGAACCGGAGCTGGA	3240
Db	3181	CTGACAGCACTCATTTAAATCAAGAAGAGTTGGCATTTGTGGGAAGAACCGGAGCTGGA	3240
Qy	3241	AAAAGTTCCCTCATCTCAGCCCTTTTAGATTGTTCAGAACCCGGAAGTTAAATTTGGATT	3300
Db	3241	AAAAGTTCCCTCATCTCAGCCCTTTTAGATTGTTCAGAACCCGGAAGTTAAATTTGGATT	3300
Qy	3301	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAATGTCAATCAT	3360
Db	3301	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAATGTCAATCAT	3360
Qy	3361	CCTCAGGAACCTGTTTGTTCACCTGGAAACAATGAGGAACCACTGGATCCCTTTAATGAG	3420
Db	3361	CCTCAGGAACCTGTTTGTTCACCTGGAAACAATGAGGAACCACTGGATCCCTTTAATGAG	3420
Qy	3421	CACAGGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA	3480
Db	3421	CACAGGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA	3480
Qy	3481	GATCTTCTGTGTAATTTGGATGAAATAGCAGAACTCAGCAATCAGGATCCAAATTTAGTGTGGA	3540
Db	3481	GATCTTCTGTGTAATTTGGATGAAATAGCAGAACTCAGCAATCAGGATCCAAATTTAGTGTGGA	3540
Qy	3541	CAAAAGCAACTGGTGTGCTTTCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT	3600
Db	3541	CAAAAGCAACTGGTGTGCTTTCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT	3600
Qy	3601	GATGAAGCGGCGGCAATTTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG	3660
Db	3601	GATGAAGCGGCGGCAATTTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG	3660
Qy	3661	GAGAAATTTGCCCCCTCACCGCTCAACCAATTCGACACAGATTGAACCACTATTTCAC	3720
Db	3661	GAGAAATTTGCCCCCTCACCGCTCAACCAATTCGACACAGATTGAACCACTATTTCAC	3720
Qy	3721	AGCGACAAGATAATTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT	3780
Db	3721	AGCGACAAGATAATTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT	3780
Qy	3781	TTGCTGCAAAATAAAGAGAGCCTATTATTAAGATGGTGCACAACTGGGGCAAGGCGAA	3840
Db	3781	TTGCTGCAAAATAAAGAGAGCCTATTATTAAGATGGTGCACAACTGGGGCAAGGCGAA	3840
Qy	3841	GCGCTCCCTCTACTGAAACAGCAACAGTATCTTCAAAAGAAATTTCCACATATT	3900
Db	3841	GCGCTCCCTCTACTGAAACAGCAACAGTATCTTCAAAAGAAATTTCCACATATT	3900
Qy	3901	GGTCACACTGACCATGTTTACAAACACTTTCCAATGGACAGCCCTCGACCTTAACATT	3960
Db	3901	GGTCACACTGACCATGTTTACAAACACTTTCCAATGGACAGCCCTCGACCTTAACATT	3960
Qy	3961	TTGAGAGACAGCACTGTGA 3978	
Db	3961	TTGAGAGACAGCACTGTGA 3978	

RESULT 2  
US-09-930-213-287  
; Sequence 287, Application US/09930213  
; Publication No. US20030170625A1

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; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHE-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELNIGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SEKS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 287
; LENGTH: 4231
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-930-213-287

Query Match      99.9%; Score 3973.2; DB 10; Length 4231;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCTGCCGTGTACACGAGGAGTGAAGCCCAACCCGCTGCAGGACGGGAACCTCTGCTCA 60
Db 116 ATGCTGCCGTGTACACGAGGAGTGAAGCCCAACCCGCTGCAGGACGGGAACCTCTGCTCA 175

Qy 61 CGCGTGTCTTCTGGTGCTCAATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAG 120
Db 176 CGCGTGTCTTCTGGTGCTCAATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAG 235

Qy 121 GAAGATGATATGATTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180
Db 236 GAAGATGATATGATTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 295

Qy 181 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATCAGCACAGAGCCCTTCTTTTA 240
Db 296 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATCAGCACAGAGCCCTTCTTTTA 355

Qy 241 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300
Db 356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 415

Qy 301 ATTCAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTTATTAATTTT 360
Db 416 ATTCAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTTATTAATTTT 475

Qy 361 GAAATATATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 420
Db 476 GAAATATATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 535

Qy 421 CTGACTTTTTCGACGCTCATTTTGGCTATATCTGCATCATCTATATTTTATCAGTTTCAG 480
Db 536 CTGACTTTTTCGACGCTCATTTTGGCTATATCTGCATCATCTATATTTTATCAGTTTCAG 595

Qy 481 TGTCTCGGATGAGTTACGAGTAGCCATATGTCATATTTATCGGAGGCACTTCGT 540
Db 596 TGTCTCGGATGAGTTACGAGTAGCCATATGTCATATTTATCGGAGGCACTTCGT 655

Qy 541 CTTAGTAACATGCGCATGGGGAAGAACACACAGGCCAGATAGTCAATCTGCTGTCCAAT 600
Db 656 CTTAGTAACATGCGCATGGGGAAGAACACACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy 601 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGACGACCACTG 660
Db 716 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGACGACCACTG 775

Qy 661 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCTTGGTGGG 720
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Db 776 CAGGCGATCGCAGTGACTGCCCTACTCTGATGGAGATAGGAATATCGTGCTTGTCTGGG 835
Qy 721 ATGGCAGTTCTAATCATCTCTGCGCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCA 780
Db 836 ATGGCAGTTCTAATCATCTCTGCGCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCA 895
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Qy 1201 CAGCTGCCGTGAGATGTTAAAGATGGTGATGTCAGGAGATTCTGCTTTTGGGAT 1260
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Db 1376 AAGGCATCAGAGACCCCAACTCTAAAGGCTTTTCTCTTAATCTGTCAGACCTGGGGAATTG 1435
Qy 1321 TTAGCTGTGTGCGCCCGCGGGAGCAGGGAAGTCATCAGCTGTTAACTGCGCTCGG 1380
Db 1436 TTAGCTGTGTGCGCCCGCGGGAGCAGGGAAGTCATCAGCTGTTAACTGCGCTCGG 1495
Qy 1381 GAATTTGCCCCCAAGTCAACGGGCTGGTCAGCGTGCATGGAAGAAATTCCTATGCTCTCAG 1440
Db 1496 GAATTTGCCCCCAAGTCAACGGGCTGGTCAGCGTGCATGGAAGAAATTCCTATGCTCTCAG 1555
Qy 1441 CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500
Db 1556 CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615
Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTG 1560
Db 1616 AAGGAACGATATGAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTTACAGCTGTG 1675
Qy 1561 GAGGATCGTATCTGACTGTGATAGGAGATCGGGGAAACCCAGCTGAGTGGAGGGCAGAAA 1620
Db 1676 GAGGATCGTATCTGACTGTGATAGGAGATCGGGGAAACCCAGCTGAGTGGAGGGCAGAAA 1735
Qy 1621 GCACGGGTAAACCTTTCGCAAGACGATGTATCAGATGCTGACATCTATCTCCTGGACGAT 1680
Db 1736 GCACGGGTAAACCTTTCGCAAGACGATGTATCAGATGCTGACATCTATCTCCTGGACGAT 1795
Qy 1681 CCTCTCAGTGCAGTAGATCGGAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA 1740
Db 1796 CCTCTCAGTGCAGTAGATCGGAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA 1855
Qy 1741 ATTTTGATGAGAGAGATCACAATTTTATGATGACTCATCAGTTTGCAGTACCTCAAAGCTGCA 1800
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Db 1856 ATTTTGCATGAGAGATCACAAATTTTGTAGTACTCATAGTTGCGAGTACTCCTCAAAAGCTGCA 1915  
Qy 1801 AGTCAGATTCTGATATTGAAGATGGTAAATTTGGTGCAGAAAGGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTCTGATATTGAAGATGGTAAATTTGGTGCAGAAAGGGGACTTACACTGAGTTC 1975  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGAGAAAGTGAACAA 1920  
Db 1976 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGAGAAAGTGAACAA 2035  
Qy 1921 CCTCAGTTCAGGAATCCACACATCAAGGAATCGTACTCTCTCAGAGTCTTCGGTTTGG 1980  
Db 2036 CCTCAGTTCAGGAATCCACACATCAAGGAATCGTACTCTCTCAGAGTCTTCGGTTTGG 2095  
Qy 1981 TCTCAACAATCTTCTAGACCTCTCTTGAAGATGGTCTCTGAGAGCCAAAGATACAGAG 2040  
Db 2096 TCTCAACAATCTTCTAGACCTCTCTTGAAGATGGTCTCTGAGAGCCAAAGATACAGAG 2155  
Qy 2041 AATGTCCAGTTACACTATCAGAGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2100  
Db 2156 AATGTCCAGTTACACTATCAGAGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2215  
Qy 2101 TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGATTTGTCATTTCCTTAATCTCCTA 2160  
Db 2216 TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGATTTGTCATTTCCTTAATCTCCTA 2275  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTCATCTGCGCAAC 2220  
Db 2276 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTCATCTGCGCAAC 2335  
Qy 2221 AAACAAAGTATGCTAAATGTCACTGTAAATCGAGAGGAAATGTAAACCGAGAAGCTAGAT 2280  
Db 2336 AAACAAAGTATGCTAAATGTCACTGTAAATCGAGAGGAAATGTAAACCGAGAAGCTAGAT 2395  
Qy 2281 CTTAACTGGTACTTAGGAATTAATTCAGGTTTAATCTAGCTAGCTAGCTGCTTTTGGCATA 2340  
Db 2396 CTTAACTGGTACTTAGGAATTAATTCAGGTTTAATCTAGCTAGCTAGCTGCTTTTGGCATA 2455  
Qy 2341 GCAAGATCTCTATTTGGTATTCTAGCTCTCTGTTAACTCTTCAAAACTTTGCAACAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTCTAGCTCTCTGTTAACTCTTCAAAACTTTGCAACAA 2515  
Qy 2401 ATGTTTGAAGTCAATCTGAAAGCTCCGGTATTAATTTCTTGATAGAAATCCAATAGGAAGA 2460  
Db 2516 ATGTTTGAAGTCAATCTGAAAGCTCCGGTATTAATTTCTTGATAGAAATCCAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCAAAAGACATTTGGACACTTGGATGATTTTGTCTGCCGCTGACGTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCAAAAGACATTTGGACACTTGGATGATTTTGTCTGCCGCTGACGTTT 2635  
Qy 2521 TTAGATTTCAACAGACATTTGCTCAAGTGGTGTGGTGTCTCTGTGGCTGTGGCCGTG 2580  
Db 2636 TTAGATTTCAACAGACATTTGCTCAAGTGGTGTGGTGTCTCTGTGGCTGTGGCCGTG 2695  
Qy 2581 ATTCCTTTGGATTCGAATACCTTGGTTCCCTTGGAAATCAATTTTCAATTTTCTTCCGCGA 2640  
Db 2696 ATTCCTTTGGATTCGAATACCTTGGTTCCCTTGGAAATCAATTTTCAATTTTCTTCCGCGA 2755  
Qy 2641 TATTTTGGAAAGCTCAAGAGATGTGAAGCCCTGGAAATCACTCAACTCGGAGTCCAGTG 2700  
Db 2756 TATTTTGGAAAGCTCAAGAGATGTGAAGCCCTGGAAATCACTCAACTCGGAGTCCAGTG 2815  
Qy 2701 TTTTCCCACTTGTCACTCTCTCTCCAGGGGCTCTGGACCACTCCGGGATACAAAGCAGAA 2760  
Db 2816 TTTTCCCACTTGTCACTCTCTCTCCAGGGGCTCTGGACCACTCCGGGATACAAAGCAGAA 2875  
Qy 2761 GAGAGGTGTGAGGAATCTTTTGTATGACACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2820  
Db 2876 GAGAGGTGTGAGGAATCTTTTGTATGACACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2935  
Qy 2821 TTTTGTGACAGCTCCCGTGGTTCGCGTCTCGATGCGATCTGTGCAATTTTGTGTC 2880  
Db 2936 TTTTGTGACAGCTCCCGTGGTTCGCGTCTCGATGCGATCTGTGCAATTTTGTGTC 2995

Qy 2881 ATCATCGTTGCTTTGGTCCCTGATTTCTGCAAAAACTCTGGATGCGGGCAGGTTGGT 2940  
Db 2996 ATCATCGTTGCTTTGGTCCCTGATTTCTGCAAAAACTCTGGATGCGGGCAGGTTGGT 3055  
Qy 2941 TTGGACATGTCCTATGCCCCCTCACGCTCATAGGGATGTTTTCAGTGGTGTGTCGACAAAGT 3000  
Db 3056 TTGGACATGTCCTATGCCCCCTCACGCTCATAGGGATGTTTTCAGTGGTGTGTCGACAAAGT 3115  
Qy 3001 GCTGAAGTTGAGATATGATGATCTCAGTAGAAAAGGTCATTGATATACAGACCTTGA 3060  
Db 3116 GCTGAAGTTGAGATATGATGATCTCAGTAGAAAAGGTCATTGATATACAGACCTTGA 3175  
Qy 3061 AAAGAAGCACCTTGGGAATATCAGAAAAGCCACACAGCCTGCCCCCATGAAGAGTG 3120  
Db 3176 AAAGAAGCACCTTGGGAATATCAGAAAAGCCACACAGCCTGCCCCCATGAAGAGTG 3235  
Qy 3121 ATAATCTTTGACATGTAAGTCTCATGTACAGTCCAGTGGGCTCTCTGGTACTGAAGCAT 3180  
Db 3236 ATAATCTTTGACATGTAAGTCTCATGTACAGTCCAGTGGGCTCTCTGGTACTGAAGCAT 3295  
Qy 3181 CTGACAGCACTCAATTAATCAGAAAAGGTTGGCATTTGTTGGGAAGAACCGGAGCTGGA 3240  
Db 3296 CTGACAGCACTCAATTAATCAGAAAAGGTTGGCATTTGTTGGGAAGAACCGGAGCTGGA 3355  
Qy 3241 AAAAGTTCCCTCATCTCAGCCCCCTTTTAGATTGTGAGAACCCGAGGTAAAAATTTGGATT 3300  
Db 3356 AAAAGTTCCCTCATCTCAGCCCCCTTTTAGATTGTGAGAACCCGAGGTAAAAATTTGGATT 3415  
Qy 3301 GATAAGATCTTGACAACTGAATTTGGAATTTCAATGATTTAAGGAAGAAATGTCATCAT 3360  
Db 3416 GATAAGATCTTGACAACTGAATTTGGAATTTCAATGATTTAAGGAAGAAATGTCATCAT 3475  
Qy 3361 CCTCAGGAACCTGTTTGTTCACCTGGAACATGAGGAAGAACCTTGGATCCCTTTAATGAG 3420  
Db 3476 CCTCAGGAACCTGTTTGTTCACCTGGAACATGAGGAAGAACCTTGGATCCCTTTAAGGAG 3535  
Qy 3421 CACACGATGAGGAACCTGTTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTCGA 3480  
Db 3536 CACACGATGAGGAACCTGTTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTCGA 3595  
Qy 3481 GATCTTCTGGTAAAAATGGAATGGAATAGCAGAACTCAGGATCCAAATTTTAGTGTGGA 3540  
Db 3596 GATCTTCTGGTAAAAATGGAATGGAATAGCAGAACTCAGGATCCAAATTTTAGTGTGGA 3655  
Qy 3541 CAAGACAACTGGTGTGCTTGGCCAGGGCAATTTCTCAGGAAGAAATCAGATTTGATTTAT 3600  
Db 3656 CAAGACAACTGGTGTGCTTGGCCAGGGCAATTTCTCAGGAAGAAATCAGATTTGATTTAT 3715  
Qy 3601 GATGAAGCAGCGCAAAATGTTGGATCCAAAGAACCTGATGATTTAATAAAAAAATCCGG 3660  
Db 3716 GATGAAGCAGCGCAAAATGTTGGATCCAAAGAACCTGATGATTTAATAAAAAAATCCGG 3775  
Qy 3661 GAGAAATTTGCCCATCGACCGTCTAAACCATTCGACACAGATTTGAACACCATTTAGAC 3720  
Db 3776 GAGAAATTTGCCCATCGACCGTCTAAACCATTCGACACAGATTTGAACACCATTTAGAC 3835  
Qy 3721 AGCGACAAGATTAATGTTTGTAGATTGAGGAAGACTGAAGAAATATGATGAGCCGTATGTT 3780  
Db 3836 AGCGACAAGATTAATGTTTGTAGATTGAGGAAGACTGAAGAAATATGATGAGCCGTATGTT 3895  
Qy 3781 TTGCTGCAAAATAAAGAGAGCTTATTTTCAAGATGTTGCAACAACTGGGCAAGCAGAA 3840  
Db 3896 TTGCTGCAAAATAAAGAGAGCTTATTTTCAAGATGTTGCAACAACTGGGCAAGCAGAA 3955  
Qy 3841 GCGCTGCCCTCACTGAAAACAGCAAAACAGGTATATCTTCAAAAAGAAATTTATCCACATTT 3900  
Db 3956 GCGCTGCCCTCACTGAAAACAGCAAAACAGGTATATCTTCAAAAAGAAATTTATCCACATTT 4015  
Qy 3901 GGTCACTACACCATGGTTTACAAACATCTCAGGACAGCCCTCGACCTTAACTATT 3960  
Db 4016 GGTCACTACACCATGGTTTACAAACATCTCAGGACAGCCCTCGACCTTAACTATT 4075



Qy	1321	TTAGCTGTGTCGGCCCCGTCGGAGCAGGAAAGTCATCACTGTTAAAGTGCCTGTCGGG	1380
Db	1436	TTAGCTGTGTCGGCCCCGTCGGAGCAGGAAAGTCATCACTGTTAAAGTGCCTGTCGGG	1495
Qy	1381	GAATTTGGCCCCCAAGTCACGGGCTGTGTCAGCGTCGATGGAAGAAATTCCTATGTCCTCAG	1440
Db	1496	GAATTTGGCCCCCAAGTCACGGGCTGTGTCAGCGTCGATGGAAGAAATTCCTATGTCCTCAG	1555
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTAAATTTGGGAAGAAATACGAA	1500
Db	1556	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTAAATTTGGGAAGAAATACGAA	1615
Qy	1501	AAGGAACGATATGAAAAAGTCATAAAGCCTTGCTCTGAAAAAGGATTTACAGCTGTG	1560
Db	1616	AAGGAACGATATGAAAAAGTCATAAAGCCTTGCTCTGAAAAAGGATTTACAGCTGTG	1675
Qy	1561	GAGATGCTGATCTGACCTGTCATAGGAGATCGGGGAACCCAGCTGAGTGGAGGCGAGAA	1620
Db	1676	GAGATGCTGATCTGACCTGTCATAGGAGATCGGGGAACCCAGCTGAGTGGAGGCGAGAA	1735
Qy	1621	GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGAGCAT	1680
Db	1736	GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGAGCAT	1795
Qy	1681	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACATTTGTCGAACTGTGTATTTGTCAA	1740
Db	1796	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACATTTGTCGAACTGTGTATTTGTCAA	1855
Qy	1741	ATTTTGCATGAGAGATCACAAATTTTGTAGTACTCATCAGTTGTCAGTACCTCAAGAGCTGCA	1800
Db	1856	ATTTTGCATGAGAGATCACAAATTTTGTAGTACTCATCAGTTGTCAGTACCTCAAGAGCTGCA	1915
Qy	1801	AGTCAGATTTCTGATTAATGAAAGATGTTAAATGTTGTCAGAGGGGACTTACACTGAGTTC	1860
Db	1916	AGTCAGATTTCTGATTAATGAAAGATGTTAAATGTTGTCAGAGGGGACTTACACTGAGTTC	1975
Qy	1861	CTAAAAATCTGATATGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAAGTGAA	1920
Db	1976	CTAAAAATCTGATATGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAAGTGAA	2035
Qy	1921	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTG	1980
Db	2036	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTG	2095
Qy	1981	TCTCAACAACTCTTAGAACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGATACAGAG	2040
Db	2096	TCTCAACAACTCTTAGAACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGATACAGAG	2155
Qy	2041	AATGTCACAGTTACACTATCAGAGGAGAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCC	2100
Db	2156	AATGTCACAGTTACACTATCAGAGGAGAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCC	2215
Qy	2101	TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGATTGTCTCATTTTCTTATTTCTCCTA	2160
Db	2216	TATAAGAAATTAATTCAGAGCTGGTGTCTCACTGGATTGTCTCATTTTCTTATTTCTCCTA	2275
Qy	2161	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTCATCTGGGCAAC	2220
Db	2276	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTCATCTGGGCAAC	2335
Qy	2221	AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAGCTAGAT	2280
Db	2336	AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAGCTAGAT	2395
Qy	2281	CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTAGTACCTACCGTCTTTTGGCATA	2340
Db	2396	CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTAGTACCTACCGTCTTTTGGCATA	2455
Qy	2341	GCAAGATCTCTATTTGGTATTTCTAGTCTCTTAACTCTTCAACAACTTTTGCACAAACAA	2400
Db	2456	GCAAGATCTCTATTTGGTATTTCTAGTCTCTTAACTCTTCAACAACTTTTGCACAAACAA	2515
Qy	2401	ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATTTCTTTGATAGAAATCCAATAGGAAGA	2460

Db	2516	ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATTTCTTTGATAGAAATCCAATAGGAAGA	2575
Qy	2461	ATTTTAAATCGTTTCTCCAAAGACATTTGGACACATTTGGATGATTTGTCGCCCTGACGTTT	2520
Db	2576	ATTTTAAATCGTTTCTCCAAAGACATTTGGACACATTTGGATGATTTGTCGCCCTGACGTTT	2635
Qy	2521	TTAGATTTTCATCCACAGACATTTGCTACAAAGTGGTGGTGTCTCTGTGGCTGTGGCCGTG	2580
Db	2636	TTAGATTTTCATCCACAGACATTTGCTACAAAGTGGTGGTGTCTCTGTGGCTGTGGCCGTG	2695
Qy	2581	ATTCCTTGGATCGCAATACCCCTTGGTTCCCTTGGAAATCATTTTCAATTTTCTTCGGCGA	2640
Db	2696	ATTCCTTGGATCGCAATACCCCTTGGTTCCCTTGGAAATCATTTTCAATTTTCTTCGGCGA	2755
Qy	2641	TATTTTGGAAACGTCGAAGAGATGTCGAAGCGCTGGAATCTCAACTCGAGGTCCAGTG	2700
Db	2756	TATTTTGGAAACGTCGAAGAGATGTCGAAGCGCTGGAATCTCAACTCGAGGTCCAGTG	2815
Qy	2701	TTTTTCCACATTTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCAATACAAAGCAGAA	2760
Db	2816	TTTTTCCACATTTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCAATACAAAGCAGAA	2875
Qy	2761	GAGAGTGTCCAGGAACCTGTTTGTATGACACACAGGATTTTACATTCAGAGGCTTGGTCTTG	2820
Db	2876	GAGAGTGTCCAGGAACCTGTTTGTATGACACACAGGATTTTACATTCAGAGGCTTGGTCTTG	2935
Qy	2821	TTTTTGAACAGCTCCCGTGGTTCGGTCCGTCTGATGCCATCTGTGCCATGTTTCTC	2880
Db	2936	TTTTTGAACAGCTCCCGTGGTTCGGTCCGTCTGATGCCATCTGTGCCATGTTTCTC	2995
Qy	2881	ATCATCGTTCGCTTTGGGTCCTCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT	2940
Db	2996	ATCATCGTTCGCTTTGGGTCCTCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT	3055
Qy	2941	TTGGCAGTCTCTATGCGCTCACGCTCATGCGGATGTTTCACTGCGTGTGTTTCGACAAAGT	3000
Db	3056	TTGGCAGTCTCTATGCGCTCACGCTCATGCGGATGTTTCACTGCGTGTGTTTCGACAAAGT	3115
Qy	3001	GCTGAAGTTCAGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTCAA	3060
Db	3116	GCTGAAGTTCAGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTCAA	3175
Qy	3061	AAAGAACACCTTTGGGAATATCAGAAACGCCACACACAGCCTGGCCCCCATGAAGAGTG	3120
Db	3176	AAAGAACACCTTTGGGAATATCAGAAACGCCACACACAGCCTGGCCCCCATGAAGAGTG	3235
Qy	3121	ATAATCTTTGACAAATGTGAACTTTCATGTACAGTCCAGGTGGGCTCTGCTGTAATGAGCAT	3180
Db	3236	ATAATCTTTGACAAATGTGAACTTTCATGTACAGTCCAGGTGGGCTCTGCTGTAATGAGCAT	3295
Qy	3181	CTGACAGCACTCAATTAATCACAAGAAAGGTTGGCAATGTTGGGAAGAACCCGGAGCTGGA	3240
Db	3296	CTGACAGCACTCAATTAATCACAAGAAAGGTTGGCAATGTTGGGAAGAACCCGGAGCTGGA	3355
Qy	3241	AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTTCAGAACCCGGAAGGTAAATTTTGAAT	3300
Db	3356	AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTTCAGAACCCGGAAGGTAAATTTTGAAT	3415
Qy	3301	GATAAGATCTTGACAACTGAAATTTGGAATTCACGATTTAAGGAAGAAATGTCATCATATA	3360
Db	3416	GATAAGATCTTGACAACTGAAATTTGGAATTCACGATTTAAGGAAGAAATGTCATCATATA	3475
Qy	3361	CCCTCAGGAACTGTTTGTTCATCTGGGAACATGAGGAAACCTCGGATCCCTTTTAAATGAG	3420
Db	3476	CCCTCAGGAACTGTTTGTTCATCTGGGAACATGAGGAAACCTCGGATCCCTTTTAAATGAG	3535
Qy	3421	CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA	3480
Db	3536	CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA	3595
Qy	3481	GATCTTCTCGTAAAAATGGATATCTGAATTTAGCAGGAATCAGGAATCCAATTTTGTGTTGGA	3540

Db 3596 GATCTTCTGGTAAATGGATGACTGAATAGCAGAAATCAGGATCCAATTTTAGTGTGGA 3655  
 Qy 3541 CAAAGACAACCTGGTGGCTGCCAGGGCAATCTCAGGAAAAATCAGATATTGATTAAT 3600  
 Db 3656 CAAAGACAACCTGGTGGCTGCCAGGGCAATCTCAGGAAAAATCAGATATTGATTAAT 3715  
 Qy 3601 GATGAAGCGACGGCAAAATGGATGATCCCAAGAACTGATGAGTTAATACAAAAAATCCGG 3660  
 Db 3716 GATGAAGCGACGGCAAAATGGATGATCCCAAGAACTGATGAGTTAATACAAAAAATCCGG 3775  
 Qy 3661 GAGAAATTTGCCCACTGCACCGTCTAACCAATGCACACAGATTTGAACACCATTTTAC 3720  
 Db 3776 GAGAAATTTGCCCACTGCACCGTCTAACCAATGCACACAGATTTGAACACCATTTTAC 3835  
 Qy 3721 AGCACAAGATATATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
 Db 3836 AGCACAAGATATATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3895  
 Qy 3781 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGGTGCACAACTGGGCAAGGCAGAA 3840  
 Db 3896 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGGTGCACAACTGGGCAAGGCAGAA 3955  
 Qy 3841 GCCCTGCCCTCACTGAAACAGCAAAACACAGGTATACCTTCAAAAGAAATTTATCCACATATT 3900  
 Db 3956 GCCCTGCCCTCACTGAAACAGCAAAACACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4015  
 Qy 3901 GGTCACTGACACATGGTTTACAAACACTTCCAATGACAGCCCTGACCTTAACTATT 3960  
 Db 4016 GGTCACTGACACATGGTTTACAAACACTTCCAATGACAGCCCTGACCTTAACTATT 4075  
 Qy 3961 TTCGAGACAGCAGTGTGA 3978  
 Db 4076 TTCGAGACAGCAGTGTGA 4093

RESULT 4

US-10-889-503-1  
 ; Sequence 1, Application US/10889503  
 ; Publication No. US20050063968A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fox Chase Cancer Center  
 ; APPLICANT: Krüh, Gary D.  
 ; APPLICANT: Lee, Kun  
 ; APPLICANT: Belinsky, Martin G.  
 ; APPLICANT: Bain, Lisa J.  
 ; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding  
 ; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof  
 ; FILE REFERENCE: FCCC 98-02  
 ; CURRENT APPLICATION NUMBER: US/10/889,503  
 ; CURRENT FILING DATE: 2004-07-12  
 ; PRIOR APPLICATION NUMBER: US/09/647,140  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US99/06644  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079,759  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/095,153  
 ; PRIOR FILING DATE: 1998-08-03  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4231  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-889-503-1

Query Match 99.9%; Score 3973.2; DB 19; Length 4231;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ATGCTGCCCGTGTACCAAGAGGTGAAGCCCAACCGCTGACAGGACGGAACTCTGCTCA 60  
 Db 116 ATGCTGCCCGTGTACCAAGAGGTGAAGCCCAACCGCTGACAGGACGGAACTCTGCTCA 175

Qy 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTCTTTAAAAATTCGCCATAAACGGAGATTAGAG 120  
 Db 176 CGCGTGTCTTCTGGTGGCTCAATCCCTTCTTTAAAAATTCGCCATAAACGGAGATTAGAG 235  
 Qy 121 GAAGATGATATGATATTCAGTGGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGAGTTG 180  
 Db 236 GAAGATGATATGATATTCAGTGGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGAGTTG 295  
 Qy 181 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGCACAGAGCCCTTCTTTA 240  
 Db 296 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGCACAGAGCCCTTCTTTA 355  
 Qy 241 ACAAGAGCAATCATTAAGTGTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
 Db 356 ACAAGAGCAATCATTAAGTGTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 415  
 Qy 301 ATTGAGAAAAAGTGCAAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 360  
 Db 416 ATTGAGAAAAAGTGCAAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 475  
 Qy 361 GAAAAATPATGATCCCATGGATTCGTGGCTTTGAAACACAGCGTACGCTATGCCACGGTG 420  
 Db 476 GAAAAATPATGATCCCATGGATTCGTGGCTTTGAAACACAGCGTACGCTATGCCACGGTG 535  
 Qy 421 CTGACTTTTTCACGCTCATTTTGGCTATACTGCATCACTTATATTTTATCACTTCACTG 480  
 Db 536 CTGACTTTTTCACGCTCATTTTGGCTATACTGCATCACTTATATTTTATCACTTCACTG 595  
 Qy 481 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATTCGT 540  
 Db 596 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATTCGT 655  
 Qy 541 CTTAGTAAACATGGCCATGGGGAAGACAACACAGGCCAGATGATCAATCTGCTGTCCAAT 600  
 Db 656 CTTAGTAAACATGGCCATGGGGAAGACAACACAGGCCAGATGATCAATCTGCTGTCCAAT 715  
 Qy 601 GATGTGAACAGTTTGTATCAGGTGACAGTCTTCTTACACTTCCCTGGGAGGACCACTG 660  
 Db 716 GATGTGAACAGTTTGTATCAGGTGACAGTCTTCTTACACTTCCCTGGGAGGACCACTG 775  
 Qy 661 CAGCGATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGTCTGTGGG 720  
 Db 776 CAGCGATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGTCTGTGGG 835  
 Qy 721 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 780  
 Db 836 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 895  
 Qy 781 CTGAGGATTAAGGATTAATAAATGTCAGCTTCCAGGATCCAGGATCAGGACCATGAATGAAGTTATA 840  
 Db 896 CTGAGGATTAAGGATTAATAAATGTCAGCTTCCAGGATCCAGGATCAGGACCATGAATGAAGTTATA 955  
 Qy 841 ACTGGTATAAGGATTAATAAATGTCAGCTTCCAGGATCCAGGATCAGGACCATGAATGAAGTTATA 900  
 Db 956 ACTGGTATAAGGATTAATAAATGTCAGCTTCCAGGATCCAGGATCAGGACCATGAATGAAGTTATA 1015  
 Qy 901 AATTGGAAGAAGAGGAGATTCCAGATTTCTGAGAAAGTTCTCTGCCCTCAGGGGAGTGAAT 960  
 Db 1016 AATTGGAAGAAGAGGAGATTCCAGATTTCTGAGAAAGTTCTCTGCCCTCAGGGGAGTGAAT 1075  
 Qy 961 TTGGCTTCTGTTTTCAGTGCAGCAAAATCATCGTGTTCGACCTTCCACCACCTACGTG 1020  
 Db 1076 TTGGCTTCTGTTTTCAGTGCAGCAAAATCATCGTGTTCGACCTTCCACCACCTACGTG 1135  
 Qy 1021 CTCCTCCGCGAGTGTGATCACAGCCAGCCGGTGTTCGTTGGCAGTGCAGCTGTATGGGCT 1080  
 Db 1136 CTCCTCCGCGAGTGTGATCACAGCCAGCCGGTGTTCGTTGGCAGTGCAGCTGTATGGGCT 1195  
 Qy 1081 GTGCGGCTGACGGTTACCTCTTCTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC 1140  
 Db 1196 GTGCGGCTGACGGTTACCTCTTCTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC 1255



Db 3416 GATAAGATCTTGACAACTGAAATGGACTTCACGATTTAAAGGAAGAAAATGTCAATCAT 3475  
 Qy 3361 CCTCAGGAACCTGTTTGTTCACATGGACCAATGAGGAAAACCTGGATCCCTTTAATGAG 3420  
 Db 3476 CCTCAGGAACCTGTTTGTTCACATGGACCAATGAGGAAAACCTGGATCCCTTTAAGGAG 3535  
 Qy 3421 CACACGATGAGGAACCTGGAATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3480  
 Db 3536 CACACGATGAGGAACCTGGAATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3595  
 Qy 3481 GATCTTCTGTAATAATGGATACCTGATGAGGCAATCTCAGGAAAATCAGATATTGATATT 3600  
 Db 3596 GATCTTCTGTAATAATGGATACCTGATGAGGCAATCTCAGGAAAATCAGATATTGATATT 3715  
 Qy 3541 CAAAGACAACTGGTGTGCTTGCAGGGCAATCTCAGGAAAATCAGATATTGATATT 3600  
 Db 3656 CAAAGACAACTGGTGTGCTTGCAGGGCAATCTCAGGAAAATCAGATATTGATATT 3715  
 Qy 3601 GATGACGACGCGCAATGTTGATCCAGAACTGATGAGTTAATACAAAATAAATCCGG 3660  
 Db 3716 GATGACGACGCGCAATGTTGATCCAGAACTGATGAGTTAATACAAAATAAATCCGG 3775  
 Qy 3661 GAGAAATTTGCCACTGACCGTCTAACCATTCACACAGATTGAACACCATTAATTGAC 3720  
 Db 3776 GAGAAATTTGCCACTGACCGTCTAACCATTCACACAGATTGAACACCATTAATTGAC 3835  
 Qy 3721 AGCACAAGATATGGTTTATAGATTCAGGAAGACTGAAAGAAATGATGATAGCCGTATGTT 3780  
 Db 3836 AGCACAAGATATGGTTTATAGATTCAGGAAGACTGAAAGAAATGATGATAGCCGTATGTT 3895  
 Qy 3781 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGTTGCAACAACTGGGCAAGGCAGAA 3840  
 Db 3896 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGTTGCAACAACTGGGCAAGGCAGAA 3955  
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 Db 3956 GCGCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTACACATATT 4015  
 Qy 3901 GGTCACTAGCACATGGTTTACAAACACTTCCAATGGACAGCCCTCGACCTTCACTATT 3960  
 Db 4016 GGTCACTAGCACATGGTTTACAAACACTTCCAATGGACAGCCCTCGACCTTCACTATT 4075  
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 Db 4076 TTCGAGACGACCTGTGA 4093

RESULT 5  
 US-10-205-823-1  
 ; Sequence 1, Application US/10205823  
 ; Publication No. US20030108963A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Monahan, John E.  
 ; APPLICANT: Endege, Wilson O.  
 ; APPLICANT: Gannavarapu, Manjula  
 ; APPLICANT: Gorbacheva, Bella  
 ; APPLICANT: Hoersch, Sebastian  
 ; APPLICANT: Kamatkar, Shubhangi  
 ; APPLICANT: Wonsley, Angela M.  
 ; APPLICANT: Glatt, Karen  
 ; APPLICANT: Zhao, Xumei  
 ; APPLICANT: Anderson, Dustin  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
 ; FILE REFERENCE: MRI-044  
 ; CURRENT APPLICATION NUMBER: US/10/205,823  
 ; PRIOR FILING DATE: 2002-07-25  
 ; PRIOR FILING DATE: 2001-07-25  
 ; PRIOR FILING DATE: 2001-07-25  
 ; PRIOR FILING DATE: 2001-07-25

; PRIOR APPLICATION NUMBER: 60/325,020  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: 60/341,746  
 ; PRIOR FILING DATE: 2001-12-12  
 ; PRIOR APPLICATION NUMBER: 60/362,158  
 ; PRIOR FILING DATE: 2002-03-05  
 ; NUMBER OF SEQ ID NOS: 455  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 5870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-205-823-1  
 Query Match 99.9%; Score 3973.2; DB 15; Length 5870;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 Qy 61 CCGTGTCTTCTTGGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGAGATTAGAG 120  
 Db 176 CCGTGTCTTCTTGGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGAGATTAGAG 235  
 Qy 121 GAAGATGATATGATTTCAGTGTCTGCCAGAAGACCGCTCACAGACCTTGGAGAGGTTG 180  
 Db 236 GAAGATGATATGATTTCAGTGTCTGCCAGAAGACCGCTCACAGACCTTGGAGAGGTTG 295  
 Qy 181 CAAGGGTTCGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCCCTTCTTTA 240  
 Db 296 CAAGGGTTCGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCCCTTCTTTA 355  
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 Db 356 ACAAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTTCAGTTA 415  
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 Db 476 GAAAATTTATGATCCCATGGATTCTGTGGCTTTGAAACAGCGTACGCTATGCCACGGTG 535  
 Qy 421 CTGACTTTTTCACGCTCATTTTGGCTATATCTGCATCATCTTATTTTATCAGTTTCA 480  
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 Qy 541 CTTAGTAAATGATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT 600  
 Db 656 CTTAGTAAATGATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT 715  
 Qy 601 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACCACTG 660  
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 Db 776 CAGCGATCGAGTACTGCTTACTCTGATGAGATAGGAATATGCTGCTTCTGCTGGG 835  
 Qy 721 ATGGCAGTTCTTAATCACTTCTCTGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCT 780  
 Db 836 ATGGCAGTTCTTAATCACTTCTCTGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCT 895  
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 Db 896 CTGAGGAGTAAACTGCAATTTTCA CGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955



Qy 841 ACTGGTATAAGGATAAATAAATGATACGCTGGGAAAGTCAATTTCAAATCTTATTACC 900  
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 Qy 1021 CTCCTCGGAGTGTGATCAAGCAGCGCGGTGTTCTGCGAGTGACGCTGTATGGGGCT 1080  
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 Db 1256 GTGAGCATCGAAGAAATCGAGACCTTTTGTCTACTTGATGAGATATCACAGCGCAACCGT 1315  
 Qy 1201 CAGCTGCCGTGATGGTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1260  
 Db 1316 CAGCTGCCGTGATGGTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1375  
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 Db 1376 AAGGCATCAGAGACCCCACTCTCAAGGCTTTCTTTACTGTGACAGCTGGGAAATG 1435  
 Qy 1321 TTAGCTGTGTGCGCCCGTGGGAGCAGGAAAGTCACTGTTTAAAGTGCCTGCTCGGG 1380  
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 Qy 1381 GAATTTGCCCAAGTCAAGGCTGGTGCAGGCTGATGGAAGAAATGCTATGTCTCAG 1440  
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 Qy 1801 AGTCAGATCTGATATTTGAAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTC 1860  
 Db 1916 AGTCAGATCTGATATTTGAAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTC 1975  
 Qy 1861 CTAATCTGATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAA 1920  
 Db 1976 CTAATCTGATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAA 2035

Qy 1921 CCTCAGTTCAGGAATCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG 1980  
 Db 2036 CCTCAGTTCAGGAATCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG 2095  
 Qy 1981 TCTCAACAATCTTCTAGACCTCCTTGAAGATGGTCTCTGGAGAGCCAGATACAGAG 2040  
 Db 2096 TCTCAACAATCTTCTAGACCTCCTTGAAGATGGTCTCTGGAGAGCCAGATACAGAG 2155  
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 Db 2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2455  
 Qy 2341 GCAAGATCTCTATGGTATTTCTAGCTCTTGTAACTCTTCACAAACTTTGCAACAA 2400  
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 Db 3056 TTGSCACTGTCTTATGCCCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3115  
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Db 3236 ATATCTTTTACATGTCGAACTTCATGTCAGTCCAGTGGGCTCTGGTACTGAGCAT 3295
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Db 4016 GGTCACTGACCACTGGTTTACAAACACTTCCCAATGGACAGCCCTCGACCTTAACTATT 4075
Qy 3961 TTCGAGACAGCACTGTGA 3978
Db 4076 TTCGAGACAGCACTGTGA 4093

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RESULT 6

US-10-887-553A-717  
; Sequence 717, Application US/10887553A  
; Publication No. US20050085436A1  
; GENERAL INFORMATION:

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; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717
; LENGTH: 5871
; TYPE: DNA
; ORGANISM: human
; US-10-887-553A-717

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Query Match 99.9%; Score 3973.2; DB 19; Length 5871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 176 CGCGTGTCTTCTGCTGGCTCAATCCCTGCTTTAAATTCGCCATAACCGAGATTAGAG 235
Qy 121 GAAGATGATATGATTTTCAAGTGTCCAGAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180
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Qy 181 CAAGGGTTCGGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTA 240
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Qy 241 ACAAGAGCAATCAATGAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTGA 300
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Qy 421 CTGACTTTTTCACGCTCATTTTGGCTTATCTGCATCACTTATATTTTATCAGTTTCAG 480
Db 536 CTGACTTTTTCACGCTCATTTTGGCTTATCTGCATCACTTATATTTTATCAGTTTCAG 595
Qy 481 TGTGCTGGGATGAGTTTACGAGTAGCCATATGCCATAATGATTTATCGGAAAGGCACTTCGT 540
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Db 716 GATCTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGCTGGGAGGACCACTG 775
Qy 661 CAGGCGATCGCAGTGAATGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTGGG 720
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Qy 721 ATGGCAGTTCTAATCATCTTCTGCCCTTGCAGAGCTGTTTGGGAAAGTTGTTCTCATCA 780
Db 836 ATGGCAGTTCTAATCATCTTCTGCCCTTGCAGAGCTGTTTGGGAAAGTTGTTCTCATCA 895

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Qy	781	CTGAGGAGTAAAACTGCAACTTTTCA	CGGATGCCAGGATCAGGACCAATGAATGAAGTTATA	840
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Qy	841	ACTGGTATAGGATAATAAATCTACGC	CTGGGAAAGTCAATTTCAAACTTTATTACC	900
Db	956	ACTGGTATAGGATAATAAATCTACGC	CTGGGAAAGTCAATTTCAAACTTTATTACC	1015
Qy	901	AAATTGAGAAAGAGAGATTTCAAGAT	TTCTGAGAAAGTTCCTGCCCTCAGGGGATGAAT	960
Db	1016	AAATTGAGAAAGAGAGATTTCAAGAT	TTCTGAGAAAGTTCCTGCCCTCAGGGGATGAAT	1075
Qy	961	TTGGCTTCGTTTTTCACTGCAAGCAAA	ATCATCGTGTGTTGACCTTCAACCTACCGTG	1020
Db	1076	TTGGCTTCGTTTTTCACTGCAAGCAAA	ATCATCGTGTGTTGACCTTCAACCTACCGTG	1135
Qy	1021	CTCCCTCGGAGTGTGATCAGACGAGC	CGCGGTGTTCTGGGAGTGAACGCTGTATGGGGCT	1080
Db	1136	CTCCCTCGGAGTGTGATCAGACGAGC	CGCGGTGTTCTGGGAGTGAACGCTGTATGGGGCT	1195
Qy	1081	GTGGGGCTGACGGTTACCCCTCTTCT	TCCCTCAGCCATTGAGAGGGTGTACAGAGGCAATC	1140
Db	1196	GTGGGGCTGACGGTTACCCCTCTTCT	TCCCTCAGCCATTGAGAGGGTGTACAGAGGCAATC	1255
Qy	1141	GTACGATCCGAAAGATCCAGACCTTT	TGCTACTTGAATGAGATATCACAGCGCAACCGT	1200
Db	1256	GTACGATCCGAAAGATCCAGACCTTT	TGCTACTTGAATGAGATATCACAGCGCAACCGT	1315
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Db	1316	CAGCTGCGGTCAAGTGTAAAGATGGT	GTGATGTGACAGGATTTTACTGCTTTTGGGAT	1375
Qy	1261	AAGGCATCAGAGACCCCAACTCTACA	AGGCCCTTTTCTTACTGTCAGACCTGGCGAATTG	1320
Db	1376	AAGGCATCAGAGACCCCAACTCTACA	AGGCCCTTTTCTTACTGTCAGACCTGGCGAATTG	1435
Qy	1321	TTAGCTGTGGTCCGCCCGTGGGAGCA	GGGAAGTCATCACTGTTTAAAGTCGCGTCTCGGG	1380
Db	1436	TTAGCTGTGGTCCGCCCGTGGGAGCA	GGGAAGTCATCACTGTTTAAAGTCGCGTCTCGGG	1495
Qy	1381	GAATTGGCCCAAGTCAAGGCTGGTCA	GCGTGTGATGGAAGATTTGCCATGTGTCTCAG	1440
Db	1496	GAATTGGCCCAAGTCAAGGCTGGTCA	GCGTGTGATGGAAGATTTGCCATGTGTCTCAG	1555
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCT	CTGAGGAGTAAATTTTATTGGAAGAAATATGAA	1500
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Qy	1621	GCAGGGTAAACCTTGAAGAGCAGTGT	ATCAAGATCTGCATCATCTCTCCGAGCAT	1680
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Qy	1681	CCTCTCAGTGCAGTAGATGCGGAAAG	TAGCAGACACTTTGTTGGAACCTGTGTATTGTCAA	1740
Db	1796	CCTCTCAGTGCAGTAGATGCGGAAAG	TAGCAGACACTTTGTTGGAACCTGTGTATTGTCAA	1855
Qy	1741	ATTTTGCATGAGAAAGATCACAAATTT	TATGATGATCAATCAGTTGCAAGTCTCAAAAGCTGCA	1800
Db	1856	ATTTTGCATGAGAAAGATCACAAATTT	TATGATGATCAATCAGTTGCAAGTCTCAAAAGCTGCA	1915
Qy	1801	AGTCAGATTTCTGATATTTGAAGATG	GTGTAAATGTGTCAGAGGGGACTTACACTGAGTTC	1860
Db	1916	AGTCAGATTTCTGATATTTGAAGATG	GTGTAAATGTGTCAGAGGGGACTTACACTGAGTTC	1975
Qy	1861	CTAAAACTCGGTATAGATTTTGGCTC	CTCTTTTAAAGAGGATAATGAGAAAGTGAAACAA	1920

Db	1976	CTAAAACTCGGTATAGATTTTGGCTC	CTCTTTTAAAGAGGATAATGAGAAAGTGAAACAA	2035
Qy	1921	CTTCCAGTTCAGGAACTCCACACTAAG	GAATCGTACTTCTCAGAGTCTTCCGTTTGG	1980
Db	2036	CTTCCAGTTCAGGAACTCCACACTAAG	GAATCGTACTTCTCAGAGTCTTCCGTTTGG	2095
Qy	1981	TCTCAACAAATCTTTAGAACCTCTCT	TGAAAGATGGTCTCTGGAGAGCAAGATACAGAG	2040
Db	2096	TCTCAACAAATCTTTAGAACCTCTCT	TGAAAGATGGTCTCTGGAGAGCAAGATACAGAG	2155
Qy	2041	AATGTCAGTTCACACTATCAGAGGAA	ACGTTTCTGAAGGAAAGTTGGTTTCAGGCC	2100
Db	2156	AATGTCAGTTCACACTATCAGAGGAA	ACGTTTCTGAAGGAAAGTTGGTTTCAGGCC	2215
Qy	2101	TATAAGAAATTTACTTTACAGCTGGT	GTCTCACTGGAATGTCTTCAATTTCTTATCTCTTA	2160
Db	2216	TATAAGAAATTTACTTTACAGCTGGT	GTCTCACTGGAATGTCTTCAATTTCTTATCTCTTA	2275
Qy	2161	AACACTGCAGCTCAGGTTGCCATATG	TCTTCAAGATTTGGTGGCTTTTATCTGGGCAAAC	2220
Db	2276	AACACTGCAGCTCAGGTTGCCATATG	TCTTCAAGATTTGGTGGCTTTTATCTGGGCAAAC	2335
Qy	2221	AAACAAAGTATGCTAAATGTCACTGT	AAATGGAGGAGAAATGTAAACGAGAAAGCTAGAT	2280
Db	2336	AAACAAAGTATGCTAAATGTCACTGT	AAATGGAGGAGAAATGTAAACGAGAAAGCTAGAT	2395
Qy	2281	CTTTAACTGGTACTTTAGGAAATTTA	TTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Db	2396	CTTTAACTGGTACTTTAGGAAATTTA	TTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2455
Qy	2341	GCAAGATCTCTATTGGTATTCTACGT	CTCTTGTAACTCTTCAACAACTTTTGCACAAACAA	2400
Db	2456	GCAAGATCTCTATTGGTATTCTACGT	CTCTTGTAACTCTTCAACAACTTTTGCACAAACAA	2515
Qy	2401	ATGTTTGAAGTCAATCTTGAAAGCT	CCGGTATATTCTTTGATAGAAATCCAATAGGAAGA	2460
Db	2516	ATGTTTGAAGTCAATCTTGAAAGCT	CCGGTATATTCTTTGATAGAAATCCAATAGGAAGA	2575
Qy	2461	ATTTTAAATCGTTTCTCCAAAGACAT	TGGACACTTGGATGATTTTCTGCGCTCAGCGTTT	2520
Db	2576	ATTTTAAATCGTTTCTCCAAAGACAT	TGGACACTTGGATGATTTTCTGCGCTCAGCGTTT	2635
Qy	2521	TTAGATTTCAATCCAGACATTTGCTA	CAAGTGGTGGTCTCTGCTGGCTGTGCGCGCTG	2580
Db	2636	TTAGATTTCAATCCAGACATTTGCTA	CAAGTGGTGGTCTCTGCTGGCTGTGCGCGCTG	2695
Qy	2581	ATTCCTTTGGATCGCAATACCCCTTG	GGTTCCCTTTGGAATCAATTTTCAATTTTCTTCCGCGA	2640
Db	2696	ATTCCTTTGGATCGCAATACCCCTTG	GGTTCCCTTTGGAATCAATTTTCAATTTTCTTCCGCGA	2755
Qy	2641	TATTTTGTGAAACGTCAGAGATGTGA	AGGCGCTGGAATCTCAACTCCGAGTCCAGTG	2700
Db	2756	TATTTTGTGAAACGTCAGAGATGTGA	AGGCGCTGGAATCTCAACTCCGAGTCCAGTG	2815
Qy	2701	TTTTTCCCACTTGTCTCTCTCCAGGG	CGCTCTGGAACCAATCCGGGCAATACAAAGCAGAA	2760
Db	2816	TTTTTCCCACTTGTCTCTCTCCAGGG	CGCTCTGGAACCAATCCGGGCAATACAAAGCAGAA	2875
Qy	2761	GAGAGGTGTGAGAACTGTGTTGATG	CAACAGATTTTACATTCAGAGGCTTGGTTCTTG	2820
Db	2876	GAGAGGTGTGAGAACTGTGTTGATG	CAACAGATTTTACATTCAGAGGCTTGGTTCTTG	2935
Qy	2821	TTTTTGAACAGCTCCCGCTGGTTCG	CGCTCGCTGGAATGCCATCTGTGCCATTTTGTGTC	2880
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Qy	2881	ATCATCTGCTTTTGGGTCCCTGATT	CTGCAAAAACTCTGGAATCCGGGCAAGTTCGT	2940
Db	2996	ATCATCTGCTTTTGGGTCCCTGATT	CTGCAAAAACTCTGGAATCCGGGCAAGTTCGT	3055
Qy	2941	TTGGCACTGCTTATGCCCTCAGCCT	CATCGGGAATGTTTTCAGTGGTGTGTTTCGACAAAGT	3000

Db 3056 TTGSCACTGCTCTATGCCCTCAOCTCATGGGATGTTTCAGTGGTGTTCGACAAAGT 3115  
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Db 3176 AAAGAAGCACTTGGGAATATCAGAAAGCCACACAGCCTGGCCCATGAGGAGTG 3235  
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Db 3236 ATAATCTTTGACAAATGTCAACTTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGCAT 3295  
Qy 3181 CTGACAGCACTCATTAATACAAAGAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
Db 3296 CTGACAGCACTCATTAATACAAAGAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3355  
Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTTCAGAACCGGAAGGTAAATTTGGATT 3300  
Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTTCAGAACCGGAGGTAAATTTGGATT 3415  
Qy 3301 GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAAATGTCAATCATA 3360  
Db 3416 GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAAATGTCAATCATA 3475  
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Db 3476 CCTCAGGAACCTGTTTGTTCACCTGGAAACATGAGGAAAAACCTGGATCCCTTTAATGAG 3535  
Qy 3421 CACACGATGAGGAACCTGGAATCCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3480  
Db 3536 CACACGATGAGGAACCTGGAATCCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595  
Qy 3481 GATCTTCTGTAAATGGATCTGAATTTAGCAGAACTCAGGATCCAATTTTAGTGTGGA 3540  
Db 3596 GATCTTCTGTAAATGGATCTGAATTTAGCAGAACTCAGGATCCAATTTTAGTGTGGA 3655  
Qy 3541 CAAAGACAACTGTTGCTGCTGCCAGGGCAATTTCTCAGGAAAAATCAGATTAATTAATT 3600  
Db 3656 CAAAGACAACTGTTGCTGCTGCCAGGGCAATTTCTCAGGAAAAATCAGATTAATTAATT 3715  
Qy 3601 GATCAAGCGCGCAATGTGGATCCAGAACTGATGATTAATACAAAAAATAATCCGG 3660  
Db 3716 GATCAAGCGCGCAATGTGGATCCAGAACTGATGATTAATACAAAAAATAATCCGG 3775  
Qy 3661 GAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCATTAATTGAC 3720  
Db 3776 GAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCATTAATTGAC 3835  
Qy 3721 AGCGACAGATAATGGTTTGTAGATTCAGGAAGACCTGAAAGAAATATGATGAGCCGTATGTT 3780  
Db 3836 AGCGACAGATAATGGTTTGTAGATTCAGGAAGACCTGAAAGAAATATGATGAGCCGTATGTT 3895  
Qy 3781 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGTGCAACAACTGGGCAAGCGAGAA 3840  
Db 3896 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGTGCAACAACTGGGCAAGCGAGAA 3955  
Qy 3841 GCCCTGCCCCTCACTGAAACAGCAAAACAGGTATACCTTTCAAAAGAAATTTATCCACATATT 3900  
Db 3956 GCCCTGCCCCTCACTGAAACAGCAAAACAGGTATACCTTTCAAAAGAAATTTATCCACATATT 4015  
Qy 3901 GGTCACTGACCAATGGTTTACAAACACATTCCTCAATGAGACGCCCTCGACCTTAATTAATT 3960  
Db 4016 GGTCACTGACCAATGGTTTACAAACACATTCCTCAATGAGACGCCCTCGACCTTAATTAATT 4075  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 7

US-09-759-143-535

; Sequence 535, Application US/09759143  
; Patent No. US20020022248A1  
; GENERAL INFORMATION:  
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; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 535  
; LENGTH: 6082  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-759-143-535

Query Match 99.7%; Score 3966; DB 9; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGCTGCCGTGTACACGAGGTGAGCCCAACCCGCTGAGGACGCGAACCTCTGCTCA 60  
Db 186 ATGCTGCCGTGTACACGAGGTGAGCCCAACCCGCTGAGGACGCGAACCTCTGCTCA 245  
Qy 61 CGGCTGTTCTTCTGGTGGCTCAATCCCTGTTTAAAAATTGGCCATAAACGGAGATTAG 120  
Db 246 CGGCTGTTCTTCTGGTGGCTCAATCCCTGTTTAAAAATTGGCCATAAACGGAGATTAG 305  
Qy 121 GAAGATGATATGATTTCAGTGTGCTGCCAGAGAACCGCTCACAGCACCTTGGAGAGATTG 180  
Db 306 GAAGATGATATGATTTCAGTGTGCTGCCAGAGAACCGCTCACAGCACCTTGGAGAGATTG 365  
Qy 181 CAAGGTTCTGGGATAAGAGTTTAAAGAGCTGAGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 240  
Db 366 CAAGGTTCTGGGATAAGAGTTTAAAGAGCTGAGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 425  
Qy 241 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
Db 426 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 485  
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Db 486 ATTGAGAAAGTGCAAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTT 545  
Qy 361 GAAATATTCATCCCATGGATCTGTGGCTTTTGAACACAGCTACGCTATGCCACGGTG 420  
Db 546 GAAATATTCATCCCATGGATCTGTGGCTTTTGAACACAGCTACGCTATGCCACGGTG 605  
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Db 606 CTGACTTTTTCACGCTCATTTTGGCTTATCTGCTATATCTGCTATATTTTATCAGTTTCAG 665  
Qy 481 TGTCTCGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGCACTTCGT 540  
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Qy 541 CTTAGTAAATGCGGCAATGGGGAAGACAACACAGGCCAGATAGTCAATCTCTGTCCAAAT 600  
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Qy 601 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCAAGGACCACTG 660  
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Db 1866 CCTCTCAGTGCAGTATGAGTGGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTTGTCAA 1925  
Qy 1741 ATTTTGATGAGAAAGATCACAAATTTTATGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCA 1800  
Db 1926 ATTTTGATGAGAAAGATCACAAATTTTATGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCA 1985  
Qy 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGTGCAAGAGGGAATTACACTGAGTTTC 1860  
Db 1986 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGTGCAAGAGGGAATTACACTGAGTTTC 2045  
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Db 2046 CTAATAATCTGATATGATTTTGGCTCCCTTTTAAAGAAAGGATTAATGAGAAAGTGAACAA 2105  
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Db 2106 CCTCCAGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165  
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Db 2706 TTAGATTTCTATTCAGACATTTGCTCAAGTGGTGGTGTGCTCTGTGGCTGTGGCCCGTG 2765  
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Qy 3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTCCACATATT 3900  
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 Qy 3901 GGTCACTACACACATGGTTTACAAACACATTTCAATGGACAGCCCTCGACCTTAACTATT 3960  
 Db 4085 GGTCACTACACACATGGTTTACAAACACATTTCAATGGACAGCCCTCGACCTTAACTATT 4144  
 Qy 3961 TTCGAGACGACACTGTGA 3978  
 Db 4145 TTCGAGACGACACTGTGA 4162  
 RESULT 8  
 US-09-780-669-535  
 ; Sequence 535, Application US/09780669  
 ; Patent No. US20020051977A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
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 ; APPLICANT: Harlocker, Susan L.  
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 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; APPLICANT: Hural, John  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Houghton, Raymond L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.427C24  
 ; CURRENT APPLICATION NUMBER: US/09/780,669  
 ; CURRENT FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 943  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 535  
 ; LENGTH: 6082  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-780-669-535  
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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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; Sequence 535, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-535

Query Match 99.7%; Score 3966; DB 9; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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## RESULT 10

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; Sequence 535, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Rector, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-535
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Query Match									
Best Local Similarity 99.7%; Score 3966; DB 9; Length 6082;									
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;									
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Db	366	CAAGGGTTCGGGATAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTA	425						
Qy	241	ACAAGAGCAATCAATAAGTGTACTCGGAATCTTATTTAGTTTGGGAATTTTACGTTA	300						
Db	426	ACAAGAGCAATCAATAAGTGTACTCGGAATCTTATTTAGTTTGGGAATTTTACGTTA	485						
Qy	301	ATTGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAAATTAATTAATTTT	360						
Db	486	ATTGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAAATTAATTAATTTT	545						
Qy	361	GAATAATATGATCCCATGGATTCGTGGCTTTGAACACAGGTCAGCTATGCCACGGT	420						
Db	546	GAATAATATGATCCCATGGATTCGTGGCTTTGAACACAGGTCAGCTATGCCACGGT	605						
Qy	421	CTGACTTTTTCAGCGCTCAATTTTCGGCTATCTGCTCATCTATATTTTATCAGTTTCAG	480						
Db	606	CTGACTTTTTCAGCGCTCAATTTTCGGCTATCTGCTCATCTATATTTTATCAGTTTCAG	665						
Qy	481	TGTGCTGGGATAGGTTACGATAGCCATGTCATATGATTTATCGGAAGGCACTTCGT	540						
Db	666	TGTGCTGGGATAGGTTACGATAGCCATGTCATATGATTTATCGGAAGGCACTTCGT	725						
Qy	541	CTTAGTAACATGGCCATGGGGAAGACCAACACAGGCCAGATAGTCAATCTGCTGCCAAT	600						
Db	726	CTTAGTAACATGGCCATGGGGAAGACCAACACAGGCCAGATAGTCAATCTGCTGCCAAT	785						
Qy	601	GATGTGAACAAAGTTTGTATCAGTGCACAGTGTCTTACACTTCTGTCGGGACGACCACTG	660						
Db	786	GATGTGAACAAAGTTTGTATCAGTGCACAGTGTCTTACACTTCTGTCGGGACGACCACTG	845						
Qy	661	CAGGCGATCGAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTGGG	720						
Db	846	CAGGCGATCGAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTGGG	905						
Qy	721	ATGGCAGTTCTAATCATTTCTGCTGCCCTTGGAAAGCTGTTTGGGAAGTTGTTCTCATCA	780						
Db	906	ATGGCAGTTCTAATCATTTCTGCTGCCCTTGGAAAGCTGTTTGGGAAGTTGTTCTCATCA	965						
Qy	781	CTGAGGAGTAAACCTGCAACTTTTCAACGATGCCAGGATCAGGACCATGAATGAAGTTATA	840						
Db	966	CTGAGGAGTAAACCTGCAACTTTTCAACGATGCCAGGATCAGGACCATGAATGAAGTTATA	1025						
Qy	841	ACTGGTATAAGGATAATAAAATGTACGCCCTGGGAAAAGTCATTTTCAAAATCTTATTAACC	900						
Db	1026	ACTGGTATAAGGATAATAAAATGTACGCCCTGGGAAAAGTCATTTTCAAAATCTTATTAACC	1085						
Qy	901	AATTTGAGAAAGAGGAGATTTTCAAGATTTCTGAGAAAGTTCTGCTCCACAGGGGATGAAT	960						
Db	1086	AATTTGAGAAAGAGGAGATTTTCAAGATTTCTGAGAAAGTTCTGCTCCACAGGGGATGAAT	1145						
Qy	961	TTGCTTTCTGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCAACCACTACGTG	1020						
Db	1146	TTGCTTTCTGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCAACCACTACGTG	1205						
Qy	1021	CTCCTCGGCAGTGTGATCA CAGGCAGCGCGTGTTCGTGGCAGTGCAGCTGTATGGGGCT	1080						

Db	1206	CTCCTCGGCAGTGTGATCA CAGGCAGCGCGTGTTCGTGGCAGTGCAGCTGTATGGGGCT	1265						
Qy	1081	GTGGGGCTGACGGTTACCCCTTCTTCCCTCAGCCATTCAGAGGGTGTCTCAGAGCAATC	1140						
Db	1266	GTGGGGCTGACGGTTACCCCTTCTTCCCTCAGCCATTCAGAGGGTGTCTCAGAGCAATC	1325						
Qy	1141	GT CAGCATCGGAAGATCCAGACCTTTTGTCTACTTGTATGAGATATCA CAGCGCAACCGT	1200						
Db	1326	GT CAGCATCGGAAGATCCAGACCTTTTGTCTACTTGTATGAGATATCA CAGCGCAACCGT	1385						
Qy	1201	CAGCTGCCGT CAGATGTGTAAAGATGTGTGATGTG CAGGATTTTATCTGCTTTTGGGAT	1260						
Db	1386	CAGCTGCCGT CAGATGTGTAAAGATGTGTGATGTG CAGGATTTTATCTGCTTTTGGGAT	1445						
Qy	1261	AAGGCATCAGAGACCCCAACTCTCAAGGGCTTTCTTACTGT CAGACCTTGGGAAATTG	1320						
Db	1446	AAGGCATCAGAGACCCCAACTCTCAAGGGCTTTCTTACTGT CAGACCTTGGGAAATTG	1505						
Qy	1321	TTAGCTGTGGT CGGCCCGCTGGGAGCAGGGAAGTCACTGT TTAAGTCCCGTCTCGGG	1380						
Db	1506	TTAGCTGTGGT CGGCCCGCTGGGAGCAGGGAAGTCACTGT TTAAGTCCCGTCTCGGG	1565						
Qy	1381	GAATTTGCCCCAAAGTCA CGGGCTGGT CAGCGTGCATGGAAGATTTGCC TATGTCTCAG	1440						
Db	1566	GAATTTGCCCCAAAGTCA CGGGCTGGT CAGCGTGCATGGAAGATTTGCC TATGTCTCAG	1625						
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAA TATTTTATTTGGGAAGAAATACGAA	1500						
Db	1626	CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAA TATTTTATTTGGGAAGAAATACGAA	1685						
Qy	1501	AAGGAACGATATGAAAAAGTCATAAAGCTTTGTCTCTG AAAAAAGGATTTACAGCTGTG	1560						
Db	1686	AAGGAACGATATGAAAAAGTCATAAAGCTTTGTCTCTG AAAAAAGGATTTACAGCTGTG	1745						
Qy	1561	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAA ACCAGCTGAGTGGAGGGCAGAAA	1620						
Db	1746	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAA ACCAGCTGAGTGGAGGGCAGAAA	1805						
Qy	1621	GCACGGGTAAACCTTGCACAGCAGTGTATCAAGATGCTG ACATCTATCTCTCGACGAT	1680						
Db	1806	GCACGGGTAAACCTTGCACAGCAGTGTATCAAGATGCTG ACATCTATCTCTCGACGAT	1865						
Qy	1681	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTT GTTTCGAACTGTGTATTTGTCAA	1740						
Db	1866	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTT GTTTCGAACTGTGTATTTGTCAA	1925						
Qy	1741	ATTTTGATCAGGAAGATCAAAATTTTATGACTCATCAGT TGCACTACCTCAAAAGCTGCA	1800						
Db	1926	ATTTTGATCAGGAAGATCAAAATTTTATGACTCATCAGT TGCACTACCTCAAAAGCTGCA	1985						
Qy	1801	AGTCAGATTTCTGATATTTGAAGATGGTAAATTTGTCAG AAGGGGACTTACACTGAGTTC	1860						
Db	1986	AGTCAGATTTCTGATATTTGAAGATGGTAAATTTGTCAG AAGGGGACTTACACTGAGTTC	2045						
Qy	1861	CTAAAACTCGTATAGATTTTGGCTCCCTTTTAAAGAA GATATAGGAAAGTGAACAA	1920						
Db	2046	CTAAAACTCGTATAGATTTTGGCTCCCTTTTAAAGAA GATATAGGAAAGTGAACAA	2105						
Qy	1921	CCTCCAGTTC CAGGAATCCCACTAAGGAATCGTATACCT TTTCTCAGAGTCTTCGGTTTGG	1980						
Db	2106	CCTCCAGTTC CAGGAATCCCACTAAGGAATCGTATACCT TTTCTCAGAGTCTTCGGTTTGG	2165						
Qy	1981	TCTCAACAAATCTTCTAGACCTCTTGTAAAGATGGTGCT CTGGAGAGCCCAAGATACAGAG	2040						
Db	2166	TCTCAACAAATCTTCTAGACCTCTTGTAAAGATGGTGCT CTGGAGAGCCCAAGATACAGAG	2225						
Qy	2041	AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAG GAAAGTTGGTTTTTCAGGCC	2100						
Db	2226	AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAG GAAAGTTGGTTTTTCAGGCC	2285						
Qy	2101	TATAAGAAATTA TTCAGAGCTGGTGTCTACTGGATGTCTT CATTCTTCTTATTTCTCTCTA	2160						

Db 2286 TATAAGAAATTAATTCAGAGCTGGTGCTCACTGGATTGTCTTCAATTTTCTTTTCTCCTA 2345  
Qy 2161 AACCTCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTCATTAATCTGGGCAAC 2220  
Db 2346 AACACTCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTCATTAATCTGGGCAAC 2405  
Qy 2221 AACCAAGATGCTAAATGTCACTGTAATGAGGAGGAAATGTAAACCGAGAGCTAGAT 2280  
Db 2406 AACCAAGATGCTAAATGTCACTGTAATGAGGAGGAAATGTAAACCGAGAGCTAGAT 2465  
Qy 2281 CTTAACTGGTACTTAGGAATTTAATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA 2340  
Db 2466 CTTAACTGGTACTTAGGAATTTAATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA 2525  
Qy 2341 GCAAGATCTCTATGGAATTCAGTCTCTGTTTAACTCTTCAAAAATTTGGCAACAAA 2400  
Db 2526 GCAAGATCTCTATGGAATTCAGTCTCTGTTTAACTCTTCAAAAATTTGGCAACAAA 2585  
Qy 2401 ATGTTTCAGTCAATTCCTGAAGCTCCGGTATTATCTTTGATAGAAATCCAAATAGGAAGA 2460  
Db 2586 ATGTTTCAGTCAATTCCTGAAGCTCCGGTATTATCTTTGATAGAAATCCAAATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCAAAGACATTTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2520  
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Qy 2521 TTAGATTTCATCAGACATTTCTCAAGATGTTGAGTGGTGGTCTCTGTTGGCTGTGGCCGCTG 2580  
Db 2706 TTAGATTTCATCAGACATTTCTCAAGATGTTGAGTGGTGGTCTCTGTTGGCTGTGGCCGCTG 2765  
Qy 2581 ATTCCTTTGGATCGCAATACCTTGTTCCCTTGGAAATCAATTTTCAATTTTCTTGGCGGA 2640  
Db 2766 ATTCCTTTGGATCGCAATACCTTGTTCCCTTGGAAATCAATTTTCAATTTTCTTGGCGGA 2825  
Qy 2641 TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGGAATCTCAAACTCGAGTCCAGTG 2700  
Db 2826 TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGGAATCTCAAACTCGAGTCCAGTG 2885  
Qy 2701 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTTGGAACCATCCGGGCAATCAAAAGAGAA 2760  
Db 2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTTGGAACCATCCGGGCAATCAAAAGAGAA 2945  
Qy 2761 GAGAGGTGTGAGGAACGTTTGTATGACACACAGGATTTACATTCAGAGGCTTGTTCTTG 2820  
Db 2946 GAGAGGTGTGAGGAACGTTTGTATGACACACAGGATTTACATTCAGAGGCTTGTTCTTG 3005  
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Db 3006 TTTTGTGACAACTGCCGCTGGTTCGCCGCTCGTCTGGATGCCATCTGTGCCATGTTTGTG 3065  
Qy 2881 ATCATCGTTGGCTTTGGGTCCTGATTCCTGGCAAAAACTCTGGATCGGGCAGGTTGGT 2940  
Db 3066 ATCATCGTTGGCTTTGGGTCCTGATTCCTGGCAAAAACTCTGGATCGGGCAGGTTGGT 3125  
Qy 2941 TTGGCACTGTCTATGCCCTCACGCTCATGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3000  
Db 3126 TTGGCACTGTCTATGCCCTCACGCTCATGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3185  
Qy 3001 GCTGAAAGTGTAGAAATATGATGATCTCAGTAGAAAGGGTCAATTTGAATACACAGACCTTGAA 3060  
Db 3186 GCTGAAAGTGTAGAAATATGATGATCTCAGTAGAAAGGGTCAATTTGAATACACAGACCTTGAA 3245  
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Db 3246 AAAGAAGCACTTTGGGAATATCAGAAACGCCCAACACAGGCTGGCCCGCATGAAGAGGTG 3305  
Qy 3121 ATATCTTTGCAATGTGAACCTTCATGTACAGTCCAGTGGGCTCTGTGTACTCGAAGCAT 3180  
Db 3306 ATATCTTTGCAATGTGAACCTTCATGTACAGTCCAGTGGGCTCTGTGTACTCGAAGCAT 3365  
Qy 3181 CTGACAGCACTCATTTAAATCAAGAAAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
Db 3366 CTGACAGCACTCATTTAAATCAAGAAAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3425

Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTTCTCAGAACCCGAGGTAATAATTTGGATT 3300  
Db 3426 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTTCTCAGAACCCGAGGTAATAATTTGGATT 3485  
Qy 3301 GATAAGATCTTGACAACTGAAATTTGGAATTTACAGATTTAAAGGAAGAAAATGTCAATCATA 3360  
Db 3486 GATAAGATCTTGACAACTGAAATTTGGAATTTACAGATTTAAAGGAAGAAAATGTCAATCATA 3545  
Qy 3361 CCTCAGGAACTGTGTTGTTTCACTGGAAACAATGAGGAAAAAATCTGGATCCCTTTAATGAG 3420  
Db 3546 CCTCAGGAACTGTGTTGTTTCACTGGAAACAATGAGGAAAAAATCTGGATCCCTTTAATGAG 3605  
Qy 3421 CACAGGATGAGNACTGTGGAATGCTTACAGAGGTACAACCTTAAGAAAAAATCCATTGAA 3480  
Db 3606 CACAGGATGAGNACTGTGGAATGCTTACAGAGGTACAACCTTAAGAAAAAATCCATTGAA 3665  
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Db 3666 GATCTTCTCGTAAAAATGGATACTGAATTAGCAGAAATCAGGATCCCAATTTTAGTGTGGA 3725  
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Qy 3601 GATGAGCGGACGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3660  
Db 3786 GATGAGCGGACGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3844  
Qy 3661 GAGAAATTTGCCCACTGCACCGTGAACCAATTTGCACACAGATTTGAACACCAATTTTAC 3720  
Db 3845 GAGAAATTTGCCCACTGCACCGTGAACCAATTTGCACACAGATTTGAACACCAATTTTAC 3904  
Qy 3721 AGCGACAAAGATAATGTTTGTAGATTTAGGAAAGCTGAAAGATATGATGAGCCGTATGTT 3780  
Db 3905 AGCGACAAAGATAATGTTTGTAGATTTAGGAAAGCTGAAAGATATGATGAGCCGTATGTT 3964  
Qy 3781 TTGCTGCAAAATTAAGAGAGCCCTATTTTCAAGATGTCACAACTGGGCAAGGCGAGAA 3840  
Db 3965 TTGCTGCAAAATTAAGAGAGCCCTATTTTCAAGATGTCACAACTGGGCAAGGCGAGAA 4024  
Qy 3841 GCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 3900  
Db 4025 GCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4084  
Qy 3901 GGTCACTCAACACATGTTTCAAAACATCTTCAATGGACAGCCCTCGACCTTAACTATT 3960  
Db 4085 GGTCACTCAACACATGTTTCAAAACATCTTCAATGGACAGCCCTCGACCTTAACTATT 4144  
Qy 3961 TTCGAGACGACCTGTGA 3978  
Db 4145 TTCGAGACGACCTGTGA 4162

## RESULT 11

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; Sequence 535, Application US/09895814  
; Publication No. US20020193296A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.



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; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C36
; CURRENT APPLICATION NUMBER: US/09/895.814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-814-535

Query Match          99,7%; Score 3966; DB 9; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGCTGCCGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGGGAACCTCTGCTCA 60
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Qy 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTGTTAAATFTGCCATAAACGAGATTAGAG 120
Db 246 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTGTTAAATFTGCCATAAACGAGATTAGAG 305

Qy 121 GAGATCATATGATTTCAGTCTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGATTG 180
Db 306 GAGATCATATGATTTCAGTCTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGATTG 365

Qy 181 CAAGGGTTCCTGGGATAAAGATTTTAAAGCTGAGATGACGACAGAGACCTTCTTTTA 240
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Qy 241 ACAAGCAATCATPAAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTACGTTA 300
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Db 486 ATTGAGAAAGTGCCTAAGTAATCCAGCCATATTTTGGGAAATTTATTAATTTT 545

Qy 361 GAAATTTATGATCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCTATGCCCGGTG 420
Db 546 GAAATTTATGATCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCTATGCCCGGTG 605

Qy 421 CTGACTTTTTCAGCTCATTTTGGCTATATCTGCATCACTTATTTTATCAGTTTCAG 480
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Db 786 GATGTGAACAAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCTGGGAGGACCACTG 845

Qy 661 CAGCGATCCGAGTACTGCCCTACTCTGATGAGATAGAGATATCTGCTGCTGGG 720
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Qy 781 CTGAGGAGTAAACTGCAACTTTTACCGATGCCAGGATCAGGACCATGAATGAAGTTTATA 840
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Qy 841 ACTGATATAAGGATAAATAAAATCTACGCCCTGGGAAAAGTCATTTTCAAACTTTATTACC 900
Db 1026 ACTGATATAAGGATAAATAAAATCTACGCCCTGGGAAAAGTCATTTTCAAACTTTATTACC 1085

Qy 901 AATTGTGAGAAAGAGGAGATTTCCAAGATTCTGAGAAAGTTTCTCCCTCAGGGGATGAAT 960
Db 1086 AATTGTGAGAAAGAGGAGATTTCCAAGATTCTGAGAAAGTTTCTCCCTCAGGGGATGAAT 1145

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Db 1326 GTGAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGAATGAGATATCACAGCGCAACCGT 1385

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Db 1746 GAGATGCTGATCTGACTGTGATAGGATCGGGGACCAAGTGTGAGTGGAGGCGAGAA 1805

Qy 1621 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680
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Qy 1741 ATTTTGCATGAGAGATCACAAATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1926 ATTTTGCATGAGAGATCACAAATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1985

Qy 1801 AGTCAGATTCTGATATTTGAAAGATGTTAAATGCTGTCAGAAAGGGGACTTACACTGAGTTC 1860

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1986 AGTCAGATTCTGATATTGAAGATGGTAAATGGTCAGAGGGGACTTACACTGAGTTC 2045  
1861 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAAACAA 1920  
2046 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAAACAA 2105  
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2106 CCTCCAGTCCAGAACTCCACACTAAGAACTGTAACCTTCTCAGAGTCTTCGGTTGG 2165  
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2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAAGCTAGAT 2465  
2281 CTTAACTGGTACTTTAGAAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGGCATA 2340  
2466 CTTAACTGGTACTTTAGAAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGGCATA 2525  
2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTGTTAACTCTTCAACAACTTTGCAACAA 2400  
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2586 ATGTTTCAGTCAATTTGAAAGCTCCGGTATATTCTTTGATAGAAATCAATAGGAAGA 2645  
2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCGCTGACGTTT 2520  
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2581 ATTCCTTTGGATCGCAATACCTTGGTTCCCTTGGAAATCAATTTTCATTTTCTTCGCGGA 2640  
2766 ATTCCTTTGGATCGCAATACCTTGGTTCCCTTGGAAATCAATTTTCATTTTCTTCGCGGA 2825  
2641 TATTTTGTGAAACGTCAGAGATGTGAAGCCCTGGAATCTACAACTCGAGTCCAGTG 2700  
2826 TATTTTGTGAAACGTCAGAGATGTGAAGCCCTGGAATCTACAACTCGAGTCCAGTG 2885  
2701 TTTTCCCACTTGTCACTCTCTCCAGGGGCTCTGGACCACTCCGGGCATACAAAGCAGAA 2760  
2886 TTTTCCCACTTGTCACTCTCTCCAGGGGCTCTGGACCACTCCGGGCATACAAAGCAGAA 2945  
2761 GAGAGGTGTCAGGAACTGTTTGTATGCAACACAGGATTTACATTCAGAGGCTTGGTTCTTG 2820  
2946 GAGAGGTGTCAGGAACTGTTTGTATGCAACACAGGATTTACATTCAGAGGCTTGGTTCTTG 3005  
2821 TTTTGTGCAAGCTCCGCTGGTTTGGCCGTCTGATGCAATCTGTGCCATGTTTGTG 2880  
3006 TTTTGTGCAAGCTCCGCTGGTTTGGCCGTCTGATGCAATCTGTGCCATGTTTGTG 3065  
2881 ATCATCGTTTGGCTTCCCTGATTTCTGGCAAAACCTCTGGATCGCGGACAGTTGGT 2940

3066 ATCATCGTTTGGCTTCCCTGATTTCTGGCAAAACCTCTGGATCGCGGACAGTTGGT 3125  
2941 TTGGCACTGCTCTATGCTCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
3126 TTGGCACTGCTCTATGCTCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3185  
3001 GCTGAAAGTTTGAGAAATGATGATCTCAGTAGAAAGGGTCAATGAATACACAGACCTTTGAA 3060  
3186 GCTGAAAGTTTGAGAAATGATGATCTCAGTAGAAAGGGTCAATGAATACACAGACCTTTGAA 3245  
3061 AAAGAGACCTTTGGGAATATCAGAAACGCCACACAGCTGGCCCTCTGGTACTGGAAGAGTG 3120  
3246 AAAGAGACCTTTGGGAATATCAGAAACGCCACACAGCTGGCCCTCTGGTACTGGAAGAGTG 3305  
3121 ATAACTTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGGAAGCAT 3180  
3306 ATAACTTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGGAAGCAT 3365  
3181 CTGACAGCACTCAATTAATCACAAGAAAGGTTGGCAATCTGTGGAGAAACCGGAGCTTGA 3240  
3366 CTGACAGCACTCAATTAATCACAAGAAAGGTTGGCAATCTGTGGAGAAACCGGAGCTTGA 3425  
3241 AAAAGTTTCCCTCATCTCAGCCCTTTTGTAGATTTGTGAGAACCCGAGGTTAAATTTGGATT 3300  
3426 AAAAGTTTCCCTCATCTCAGCCCTTTTGTAGATTTGTGAGAACCCGAGGTTAAATTTGGATT 3485  
3301 GATAAGATCTTGACAACTGAAATTTGACTTTCAGATTTTAAGGAAGAAATTTCAATCATA 3360  
3486 GATAAGATCTTGACAACTGAAATTTGACTTTCAGATTTTAAGGAAGAAATTTCAATCATA 3545  
3361 CCTCAGGAACCTGTTTGTCTGGAACCAATGAGGAAACCTCTGGATCCCTTTAATGAG 3420  
3546 CCTCAGGAACCTGTTTGTCTGGAACCAATGAGGAAACCTCTGGATCCCTTTAATGAG 3605  
3421 CACACGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCAATTTGAA 3480  
3606 CACACGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCAATTTGAA 3665  
3481 GATCTTCTGGTAAATGGATCTGAATTAGCAGATCAGATCCATTTTGTAGTTGGA 3540  
3666 GATCTTCTGGTAAATGGATCTGAATTAGCAGATCAGATCCATTTTGTAGTTGGA 3725  
3541 CAAAGACAACTGCTGCTGCTGCGAGGCAATTTCTCAGGAAATACAGATATTGATTTATT 3600  
3726 CAAAGACAACTGCTGCTGCTGCGAGGCAATTTCTCAGGAAATACAGATATTGATTTATT 3785  
3601 GATGAAGCGACGGCAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAATCCGG 3660  
3786 GATGAAGCGACGGCAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAATCCGG 3844  
3661 GAGAAATTTGCCCACTGCACTGCTTAACCATTTGCAACAGATTTGAACCATTTATTGAC 3720  
3845 GAGAAATTTGCCCACTGCACTGCTTAACCATTTGCAACAGATTTGAACCATTTATTGAC 3904  
3721 AGCGCAAGATTAATGTTTGTAGATTTAGGAAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
3905 AGCGCAAGATTAATGTTTGTAGATTTAGGAAAGACTGAAAGAAATATGATGAGCCGTATGTT 3964  
3781 TTGCTGCAAAATTAAGAGAGCCCTATTTTTACAAGATGGTGAACAACTGGGCAAGCGAGAA 3840  
3965 TTGCTGCAAAATTAAGAGAGCCCTATTTTTACAAGATGGTGAACAACTGGGCAAGCGAGAA 4024  
3841 GCGCTGCCCTCACTGAAACAGCAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 3900  
4025 GCGCTGCCCTCACTGAAACAGCAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4084  
3901 GGTCACTGACCACTGTTTACAAACACTTTCCAATGCAAGCCCTCGACCTTAACTATT 3960  
4085 GGTCACTGACCACTGTTTACAAACACTTTCCAATGCAAGCCCTCGACCTTAACTATT 4144  
3961 TTGAGACAGCACTGTGA 3978  
4145 TTGAGACAGCACTGTGA 4162

RESULT 12  
US-10-012-896-535  
; Sequence 535, Application US/10012896  
; Publication No. US20020183251A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Wantanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C27  
; CURRENT APPLICATION NUMBER: US/10/012,896  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 1011  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 535  
; LENGTH: 6082  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-012-896-535

Query Match 99.7%; Score 3966; DB 13; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1	ATGCTGCCGTGTACACGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA	60
Db	186	ATGCTGCCGTGTACACGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA	245
Qy	61	CGGTGTCTTCGTGGCTCAATCCCTTGTTHAAATTTGGCCATAACGGAGATTAGAG	120
Db	246	CGGTGTCTTCGTGGCTCAATCCCTTGTTHAAATTTGGCCATAACGGAGATTAGAG	305
Qy	121	GAAGATGATATGATTCAAGTGTCCAGAGAGCCGCTCACAGCACCTTTGGAGAGAGTTG	180
Db	306	GAAGATGATATGATTCAAGTGTCCAGAGAGCCGCTCACAGCACCTTTGGAGAGAGTTG	365
Qy	181	CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATCTTATTTTGGGAAATTTACGTTA	240
Db	366	CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATCTTATTTTGGGAAATTTACGTTA	425
Qy	241	ACAAGCAATCATAAAGTGTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA	300
Db	426	ACAAGCAATCATAAAGTGTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA	485
Qy	301	ATTGAGGAAGTGCAGAGTAATCCAGCCCATATTTTGGGAAATTTTATTAATTTT	360
Db	486	ATTGAGGAAGTGCAGAGTAATCCAGCCCATATTTTGGGAAATTTTATTAATTTT	545
Qy	361	GAATAATTATGATCCCATGGATTCTGTGGCTTTTGAACACAGCGTACGCTATGCCACGGTG	420

Db	546	GAATAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG	605
Qy	421	CTGACTTTTTCGACGCTCATTTTGGCTATATCTGATCATCACTATATTTTATCAGGTTGAG	480
Db	606	CTGACTTTTTCGACGCTCATTTTGGCTATATCTGATCATCACTATATTTTATCAGGTTGAG	665
Qy	481	TGTGCTGGGATGAGTTTACGAGTAGCCATATGTCATATGATTTATCGGAAGCACTTCGT	540
Db	666	TGTGCTGGGATGAGTTTACGAGTAGCCATATGTCATATGATTTATCGGAAGCACTTCGT	725
Qy	541	CTTAGTAACATGCGCCATGCGGGAAGACAACACACAGCCAGATAGTCAATCTGCTGCCAAT	600
Db	726	CTTAGTAACATGCGCCATGCGGGAAGACAACACACAGCCAGATAGTCAATCTGCTGCCAAT	785
Qy	601	GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGCGGAGGACCACTG	660
Db	786	GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGCGGAGGACCACTG	845
Qy	661	CAGCGCATCGCAGTGACTGCGCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTCTGG	720
Db	846	CAGCGCATCGCAGTGACTGCGCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTCTGG	905
Qy	721	ATGCGACTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA	780
Db	906	ATGCGACTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA	965
Qy	781	CTGAGGAGTAAACTGCAACTTTTACCGATGCCAGGATCAGGACCATGAATGAAGTTATA	840
Db	966	CTGAGGAGTAAACTGCAACTTTTACCGATGCCAGGATCAGGACCATGAATGAAGTTATA	1025
Qy	841	ACTGGTATAAGGATAATAAAATGACGCTCGGGAAGTCAATTTCAAATCTTATTAACC	900
Db	1026	ACTGGTATAAGGATAATAAAATGACGCTCGGGAAGTCAATTTCAAATCTTATTAACC	1085
Qy	901	AATTTGAGAAGAAGGAGATTTCAGATTCTGAGAAAGTTCTCTGCCCTCAGGGGATGAAT	960
Db	1086	AATTTGAGAAGAAGGAGATTTCAGATTCTGAGAAAGTTCTCTGCCCTCAGGGGATGAAT	1145
Qy	961	TTGGCTTCGTTTTCAGTGAAGCAAAATCATCGTGTGTTGTGACCTTCAACCACTACG	1020
Db	1146	TTGGCTTCGTTTTCAGTGAAGCAAAATCATCGTGTGTTGTGACCTTCAACCACTACG	1205
Qy	1021	CTCTCGGCAAGTGTGATCACAGCCGCGGTGTTCTGTGGCAGTGACGCTGATGGGGCT	1080
Db	1206	CTCTCGGCAAGTGTGATCACAGCCGCGGTGTTCTGTGGCAGTGACGCTGATGGGGCT	1265
Qy	1081	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTCTCAGAGGCAATC	1140
Db	1266	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTCTCAGAGGCAATC	1325
Qy	1141	GTGAGCATCGAAGATCCAGACCTTTTGTCTACTTGTATGATGATATCACAGCGCAACCGT	1200
Db	1326	GTGAGCATCGAAGATCCAGACCTTTTGTCTACTTGTATGATGATATCACAGCGCAACCGT	1385
Qy	1201	CAGCTGCGGTGAGATGTTAAAGATGTTGATGTCAGGATTTTACTGCTTTTGGAT	1260
Db	1386	CAGCTGCGGTGAGATGTTAAAGATGTTGATGTCAGGATTTTACTGCTTTTGGAT	1445
Qy	1261	AAGGCATCAGAGACCCCACTCTCAAGGCTTTCTTTTACTGTCTCAGACCTTGGGCAATTG	1320
Db	1446	AAGGCATCAGAGACCCCACTCTCAAGGCTTTCTTTTACTGTCTCAGACCTTGGGCAATTG	1505
Qy	1321	TTAGCTGTGTGCGGCGGCGGAGGAGGAGTCACTACCTGTTAGTGCCTGCTCGG	1380
Db	1506	TTAGCTGTGTGCGGCGGCGGAGGAGGAGTCACTACCTGTTAGTGCCTGCTCGG	1565
Qy	1381	GAATTGGCCCAAGTCAAGGCTGGTGGGAGGAGGAGTCACTGCTATGCTCTCAG	1440
Db	1566	GAATTGGCCCAAGTCAAGGCTGGTGGGAGGAGGAGTCACTGCTATGCTCTCAG	1625
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1500

Db 1626 CAGCCCTGGGTGTTCTCGGGAACCTCAGGAGTAATAATTTTATTTTGGGAAGAAATACGAA 1685  
Qy 1501 AAGGAACGATATGAAAAAGTCATAAAGGCTTGCTCTCTGAAAAAGGATTTACAGCTGTTG 1560  
Db 1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGCTCTCTGAAAAAGGATTTACAGCTGTTG 1745  
Qy 1561 GAGGATGCTGATCTGACCTGTGATAGGAGATCGGGGAACCAACGCTGAGTGGAGGSCAGAAA 1620  
Db 1746 GAGGATGCTGATCTGACCTGTGATAGGAGATCGGGGAACCAACGCTGAGTGGAGGSCAGAAA 1805  
Qy 1621 GCACGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGAGCAT 1680  
Db 1806 GCACGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGAGCAT 1865  
Qy 1681 CCTCTAGTCAGTAGATGCGGAAGTTAGCAGACACACTTGTTCGAACTGTGTATTTGTCAA 1740  
Db 1866 CCTCTAGTCAGTAGATGCGGAAGTTAGCAGACACACTTGTTCGAACTGTGTATTTGTCAA 1925  
Qy 1741 ATTTTGATCAGAGAGATCACAATTTTATAGTGACTCATCAGTTGCAAGTACCTCAAGCTGCA 1800  
Db 1926 ATTTTGATCAGAGAGATCACAATTTTATAGTGACTCATCAGTTGCAAGTACCTCAAGCTGCA 1985  
Qy 1801 AGTCAGATTTCTGATATTTGAAAGATGTAATAATGCTGCAAGGGGACTTACACTGAGTTC 1860  
Db 1986 AGTCAGATTTCTGATATTTGAAAGATGTAATAATGCTGCAAGGGGACTTACACTGAGTTC 2045  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGNATAGAGGAAAGTGAAACAA 1920  
Db 2046 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGNATAGAGGAAAGTGAAACAA 2105  
Qy 1921 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
Db 2106 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165  
Qy 1981 TCTCAACAATCTCTAGACCCCTCTGAAAGATGGTCTCTCGAGAGCCCAAGATACAGAG 2040  
Db 2166 TCTCAACAATCTCTAGACCCCTCTGAAAGATGGTCTCTCGAGAGCCCAAGATACAGAG 2225  
Qy 2041 AATGTCACGTTACACTATACAGAGGAGAACGTTCTGAAAGAAAGTTGGTTTCAGGCC 2100  
Db 2226 AATGTCACGTTACACTATACAGAGGAGAACGTTCTGAAAGAAAGTTGGTTTCAGGCC 2285  
Qy 2101 TATAAGAAATTAATTCAGAGCTGGTGCTCAGTGAATGCTCTCATTTTCTTATTTCTCTTA 2160  
Db 2286 TATAAGAAATTAATTCAGAGCTGGTGCTCAGTGAATGCTCTCATTTTCTTATTTCTCTTA 2345  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTTCATATCGGSCAAAC 2220  
Db 2346 AACACTGCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTTCATATCGGSCAAAC 2405  
Qy 2221 AACAAAGTATGCTAAATGTACACTGTAAATGGAGGAGGAAATGTAAACGAGAGCTAGAT 2280  
Db 2406 AACAAAGTATGCTAAATGTACACTGTAAATGGAGGAGGAAATGTAAACGAGAGCTAGAT 2465  
Qy 2281 CTTAACTGGTACTTAGGAAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGCATA 2340  
Db 2466 CTTAACTGGTACTTAGGAAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGCATA 2525  
Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTCACAAACTTTGCAACAAAA 2400  
Db 2526 GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTCACAAACTTTTGCACAAAA 2585  
Qy 2401 ATGTTTGAAGTCAATCTGAAAGCTCCGGTATTTATTTCTTGTAGTAAATCCATAGGAAGA 2460  
Db 2586 ATGTTTGAAGTCAATCTGAAAGCTCCGGTATTTATTTCTTGTAGTAAATCCATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCAAGACATTTGGACACTTTGGATGATTTGCTGCGCTCAGCTTT 2520  
Db 2646 ATTTTAAATCGTTTCTCAAGACATTTGGACACTTTGGATGATTTGCTGCGCTCAGCTTT 2705  
Qy 2521 TTAGATTTTCACAGACATTTGCTACAAGTGGTGGTGGTCTCTGCTGGCTGGCCGCTG 2580  
Db 2706 TTAGATTTTCACAGACATTTGCTACAAGTGGTGGTGGTCTCTGCTGGCTGGCCGCTG 2765

Qy 2581 ATTCTTGGATCGCAATACCCCTTGGTTCCCTTGGATCATTTTTCATTTTCTTCGSCGA 2640  
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Qy 2701 TTTTCCACATTTGTCACTTCTCTCAGGGGCTCTGGACCATTCGGGCAATCAAAAGCAAA 2760  
Db 2886 TTTTCCACATTTGTCACTTCTCTCAGGGGCTCTGGACCATTCGGGCAATCAAAAGCAAA 2945  
Qy 2761 GAGAGTGTCAAGNACTGTTTGTATGACACACAGGATTTACATTCAGAGGCTTGTTCTTG 2820  
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Qy 3061 AAGAAGACCTTTGGGAATATCAGAAACGCCACACAGCTGGCCCCCATGAAAGAGTG 3120  
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Qy 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTAGAATTTGTACAGAACCCGAGGTAAAAATTTGGATT 3300  
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Qy 3541 CAAAGACAACTGGTGTGCTTGGCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT 3600  
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Db 3786 GATGAAGCGACGGCAATTTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3844

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QY 3721 AGCGACAAGATTAATGTTTTAGATTTCAGAGAGACTGAAAGAAATATGATGAGCCGTATGTT 3780
DB 3905 AGCGACAAGATTAATGTTTTAGATTTCAGAGAGACTGAAAGAAATATGATGAGCCGTATGTT 3964
QY 3781 TTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCACCAACTGGGCAAGGCAGAA 3840
DB 3965 TTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCACCAACTGGGCAAGGCAGAA 4024
QY 3841 GCCGTGCCCTCAGTGAACAGCAAAACAGGTATATCTTCAAAAAGAAATATTCACATATT 3900
DB 4025 GCCGTGCCCTCAGTGAACAGCAAAACAGGTATATCTTCAAAAAGAAATATTCACATATT 4084
QY 3901 GGTCACTGACCACTGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACATT 3960
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QY 3961 TTCGAGACAGCACTGTGA 3978
DB 4145 TTCGAGACAGCACTGTGA 4162

RESULT 13
US-10-010-940-535
; Sequence 535, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-940-535

Query Match 99.7%; Score 3966; DB 14; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGCTGCCCGTGTACAGAGAGGTGAAGCCCAACCGCTGCGAGGACGCAACCTCTGCTCA 60
DB 186 ATGCTGCCCGTGTACAGAGAGGTGAAGCCCAACCGCTGCGAGGACGCAACCTCTGCTCA 245
QY 61 CGCGTGTCTTCTGCTGCTCAATCCCTGTTTAAATTTGGCCATAAAGCAGATTAGAG 120
DB 246 CGCGTGTCTTCTGCTGCTCAATCCCTGTTTAAATTTGGCCATAAAGCAGATTAGAG 305
QY 121 GAAGATGATATGATTTCAGTGTCTGCCAGAGACCGCTCAGACACCTTTGGAGAGAGTTG 180
DB 306 GAAGATGATATGATTTCAGTGTCTGCCAGAGACCGCTCAGACACCTTTGGAGAGAGTTG 365
QY 181 CAAGGGTCTGGGATAAAGAGTTTAAAGACTGAGAAATGACGACAGAACCTTCTTTA 240
DB 366 CAAGGGTCTGGGATAAAGAGTTTAAAGACTGAGAAATGACGACAGAACCTTCTTTA 425
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QY 241 ACAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTTAGTTTGGGAAATTTTACGTGA 300
DB 426 ACAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTTAGTTTGGGAAATTTTACGTGA 485
QY 301 ATTGAGGAAAGTGCACCAAGTAATTCAGCCCAATATTTTGGGAAATTTTAAATTTATTTT 360
DB 486 ATTGAGGAAAGTGCACCAAGTAATTCAGCCCAATATTTTGGGAAATTTTAAATTTATTTT 545
QY 361 GAAATTTATGATCCCATGATTTCTGTGGCTTTTGAACACAGCGTAGCCCTATGCCACGGTG 420
DB 546 GAAATTTATGATCCCATGATTTCTGTGGCTTTTGAACACAGCGTAGCCCTATGCCACGGTG 605
QY 421 CTGACTTTTTTGCACGCTCATTTTGGCTATCTGTCATCACTTATATTTTATCACGTTTCAG 480
DB 606 CTGACTTTTTTGCACGCTCATTTTGGCTATCTGTCATCACTTATATTTTATCACGTTTCAG 665
QY 481 TGTGCTGGGATGAGGTTACGATGAGCCATGTCGATATGATTTATCGGAAGCACTTCGT 540
DB 666 TGTGCTGGGATGAGGTTACGATGAGCCATGTCGATATGATTTATCGGAAGCACTTCGT 725
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DB 726 CTTAGTAACATGCGGCATGGGGAAGACACACACAGSCCAGATAGTCAATCTGCTGCCAAT 785
QY 601 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCGAGGACCACTG 660
DB 786 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCGAGGACCACTG 845
QY 661 CAGCGGATCGCAGTGACGTGCCCTACTCTGGATGGAGATAGGAATATCTGCTTCCTGGG 720
DB 846 CAGCGGATCGCAGTGACGTGCCCTACTCTGGATGGAGATAGGAATATCTGCTTCCTGGG 905
QY 721 ATGCGAGTTCTAAATCATTCTCTGCCCTTGCARAGCTGTTTGGGAAGTGTCTTCATCA 780
DB 906 ATGCGAGTTCTAAATCATTCTCTGCCCTTGCARAGCTGTTTGGGAAGTGTCTTCATCA 965
QY 781 CTGAGGAGTAAAACTGCAACTTTTCCAGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840
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QY 841 ACTGTTATAGGATTAATAAATATGATCGCTGGGAAAGTCAATTTTCAATTTATTTACC 900
DB 1026 ACTGTTATAGGATTAATAAATATGATCGCTGGGAAAGTCAATTTTCAATTTATTTACC 1085
QY 901 AATTTGAGAGAGAGGAGATTTTCAAGATTTCTGAGAGTGTCTTCCCTCAGGGGATGAAT 960
DB 1086 AATTTGAGAGAGAGGAGATTTTCAAGATTTCTGAGAGTGTCTTCCCTCAGGGGATGAAT 1145
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QY 1021 CTCCTCGGCAAGTGTGATCAGACGCGCGGTGTTCTGTCGAGTGACGCTGTATGGGCT 1080
DB 1206 CTCCTCGGCAAGTGTGATCAGACGCGCGGTGTTCTGTCGAGTGACGCTGTATGGGCT 1265
QY 1081 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGTTGTGAGAGCAATC 1140
DB 1266 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGTTGTGAGAGCAATC 1325
QY 1141 GTGAGCATCGAAGAAATCCAGACCTTTTGTGCTTCTGATGAGATATCACAGCGCAACCGT 1200
DB 1326 GTGAGCATCGAAGAAATCCAGACCTTTTGTGCTTCTGATGAGATATCACAGCGCAACCGT 1385
QY 1201 CAGCTGCCGTGAGATGTTGTAAGAAAGATGTTGATGTCAGGATTTTACTGCTTTTGGGAT 1260
DB 1386 CAGCTGCCGTGAGATGTTGTAAGAAAGATGTTGATGTCAGGATTTTACTGCTTTTGGGAT 1445
QY 1261 AAGGCATCAGAGACCCCACTCTACAGGCTTTCTTACTGTAGACCTTGGGCAATG 1320
DB 1446 AAGGCATCAGAGACCCCACTCTACAGGCTTTCTTACTGTAGACCTTGGGCAATG 1505
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Qy	1321	TTAGCTGTGGTGGCCCGCTGGGAGCAGGAAGTCATCATTGTTAAAGTCGCGTCTCGG	1380
Db	1506	TTAGCTGTGGTGGCCCGCTGGGAGCAGGAAGTCATCATTGTTAAAGTCGCGTCTCGG	1565
Qy	1381	GAATTGGCCCCAAGTCACGGGCTGGTCAAGCGTGCATGGAAGAAATGGCTATGTCTCAG	1440
Db	1566	GAATTGGCCCCAAGTCACGGGCTGGTCAAGCGTGCATGGAAGAAATGGCTATGTCTCAG	1625
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAAATATTTTATTTGGGAAGAAATAGAA	1500
Db	1626	CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAAATATTTTATTTGGGAAGAAATAGAA	1685
Qy	1501	AAGGAACGATATGAAAAGTCATAAAGCTTTGTCTCTGAAAAAGGATTTACAGCTGTG	1560
Db	1686	AAGGAACGATATGAAAAGTCATAAAGCTTTGTCTCTGAAAAAGGATTTACAGCTGTG	1745
Qy	1561	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGSCAGAAA	1620
Db	1746	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGSCAGAAA	1805
Qy	1621	GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACGAT	1680
Db	1806	GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACGAT	1865
Qy	1681	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTTGTTTGAACGTGTATTTGTCAA	1740
Db	1866	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTTGTTTGAACGTGTATTTGTCAA	1925
Qy	1741	ATTTTGCATGAGAAAGATCACAAATTTTATGATCACTCATCAGTTGCACTACCTCAAAGCTGCA	1800
Db	1926	ATTTTGCATGAGAAAGATCACAAATTTTATGATCACTCATCAGTTGCACTACCTCAAAGCTGCA	1985
Qy	1801	AGTCAGATTTCTGATTTAAAGATGGTAAATGTGTGCAAGAGGGGACTTACACTGAGTTC	1860
Db	1986	AGTCAGATTTCTGATTTAAAGATGGTAAATGTGTGCAAGAGGGGACTTACACTGAGTTC	2045
Qy	1861	CTAAATCTGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA	1920
Db	2046	CTAAATCTGTGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA	2105
Qy	1921	CCTCCAGTTCGAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG	1980
Db	2106	CCTCCAGTTCGAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG	2165
Qy	1981	TCTCAACAAATCTTACAGCCCTCTTGAAGATGGTGTCTCGAGAGCCAGATACAGAG	2040
Db	2166	TCTCAACAAATCTTACAGCCCTCTTGAAGATGGTGTCTCGAGAGCCAGATACAGAG	2225
Qy	2041	AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC	2100
Db	2226	AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC	2285
Qy	2101	TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGAATGTCTTCAATTTTCTTATTCCTTA	2160
Db	2286	TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGAATGTCTTCAATTTTCTTATTCCTTA	2345
Qy	2161	AACCTGAGCTCAGGTGCTTATGTCTTCAAGATTTGAGTGGTGGCTTTCATCTGGGCAAC	2220
Db	2346	AACCTGAGCTCAGGTGCTTATGTCTTCAAGATTTGAGTGGTGGCTTTCATCTGGGCAAC	2405
Qy	2221	AAACAAAGATGCTAAATGTACCTGTAATGAGGAGGAAATGTAACCGAGAGCTAGAT	2280
Db	2406	AAACAAAGATGCTAAATGTACCTGTAATGAGGAGGAAATGTAACCGAGAGCTAGAT	2465
Qy	2281	CTTAACTGGTACTTATAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Db	2466	CTTAACTGGTACTTATAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2525
Qy	2341	GCAAGATCTCTATTTGGTATTTCTAGCTCTCTTGTAACTTCACTTTCACAAAATTTGCAACAA	2400
Db	2526	GCAAGATCTCTATTTGGTATTTCTAGCTCTCTTGTAACTTCACTTTCACAAAATTTGCAACAA	2585
Qy	2401	ATGTTTGAGTCAAATCTCGAAAGCTCCGGTATTTATTTCTTTGATAGAAATCCAATAGGAAGA	2460

Db	2586	ATGTTTGAGTCAAATCTGAAAGCTCCGGTATTTATTTCTTTGATAGAAATCCAATAGGAAGA	2645
Qy	2461	ATTTTAAATCGTTTCTCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACGTTTT	2520
Db	2646	ATTTTAAATCGTTTCTCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACGTTTT	2705
Qy	2521	TTAGATTTTCATCAGACATTTGCTACAGTGGTGGTGGTCTCTGTGGCTGTGCGCGTG	2580
Db	2706	TTAGATTTTCATCAGACATTTGCTACAGTGGTGGTGGTCTCTGTGGCTGTGCGCGTG	2765
Qy	2581	ATTTCTTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCAATTTTCTTTCTCGGCGA	2640
Db	2766	ATTTCTTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCAATTTTCTTTCTCGGCGA	2825
Qy	2641	TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTCGAAATCTACAACTCGGAGTCCAGTG	2700
Db	2826	TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTCGAAATCTACAACTCGGAGTCCAGTG	2885
Qy	2701	TTTTCACACTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2760
Db	2886	TTTTCACACTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2945
Qy	2761	GAGAGGTGTGAGAACTGTGTTGATGCACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	2820
Db	2946	GAGAGGTGTGAGAACTGTGTTGATGCACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	3005
Qy	2821	TTTTTGACAAAGTCCCGCTGGTTCGCGTCCGCTCTGATGCCATCTGTGCCATGTTTGTG	2880
Db	3006	TTTTTGACAAAGTCCCGCTGGTTCGCGTCCGCTCTGATGCCATCTGTGCCATGTTTGTG	3065
Qy	2881	ATCATCGTTCCTTTGGGTCCCTGATTTCTGCAAAAACTCTGGATCCGGCAGGTTGGT	2940
Db	3066	ATCATCGTTCCTTTGGGTCCCTGATTTCTGCAAAAACTCTGGATCCGGCAGGTTGGT	3125
Qy	2941	TTGGCAGTCTCTATGCCCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3000
Db	3126	TTGGCAGTCTCTATGCCCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3185
Qy	3001	GCTGAAGTGGAAATATGATGATCTCAGTAGAAGGGTCAATTGATACACAGACTTGAA	3060
Db	3186	GCTGAAGTGGAAATATGATGATCTCAGTAGAAGGGTCAATTGATACACAGACTTGAA	3245
Qy	3061	AAAGAACCTTTGGGAATATCAGAACGCCACACAGCTCGGCCCATGAAGGAGTG	3120
Db	3246	AAAGAACCTTTGGGAATATCAGAACGCCACACAGCTCGGCCCATGAAGGAGTG	3305
Qy	3121	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCCCTCTGGTACTGAAGCAT	3180
Db	3306	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCCCTCTGGTACTGAAGCAT	3365
Qy	3181	CTGACAGCATCTATTAATCACAAGAAAGGTTGGCAATTGCGGAAGAACCCGGAGCTGGA	3240
Db	3366	CTGACAGCATCTATTAATCACAAGAAAGGTTGGCAATTGCGGAAGAACCCGGAGCTGGA	3425
Qy	3241	AAAAGTCCCTCATCTCAGCCCTTTTAGATTGTTCAGAACCCGGAAGGTAATAATTTGGATT	3300
Db	3426	AAAAGTCCCTCATCTCAGCCCTTTTAGATTGTTCAGAACCCGGAAGGTAATAATTTGGATT	3485
Qy	3301	GATAAGATCTTGACAACTGAAATTTGGAATTCACGATTTAAGGAAGAAAAATGCTCAATCAT	3360
Db	3486	GATAAGATCTTGACAACTGAAATTTGGAATTCACGATTTAAGGAAGAAAAATGCTCAATCAT	3545
Qy	3361	CCTCAGGAACTGTGTTTGTTCATCTGGAACTATGAGGAAAAACCTGGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAACTGTGTTTGTTCATCTGGAACTATGAGGAAAAACCTGGATCCCTTTAATGAG	3605
Qy	3421	CACACGATGAGGAACGTGGATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA	3480
Db	3606	CACACGATGAGGAACGTGGATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA	3665
Qy	3481	GATCTTCTGGTAAAAATGGATCTGAAATTAGCAGAAATCAGGAATCCAAATTTAGTGTGGA	3540



Db 3666 GATCTTCTGCTGATACTGAATACAGAAATCAGATCCAAATTTTAGTGTGGA 3725  
Qy 3541 CAAGACAACTGGTGTGCTTCCAGGCAATTTCTCAGGAAAAATCAGATATGATATT 3600  
Db 3726 CAAGACAACTGGTGTGCTTCCAGGCAATTTCTCAGGAAAAATCAGATATGATATT 3785  
Qy 3601 GATGAAGGACGGCAATGTGGATCCAGAACTGATGATTAATAACAAAAAATCCGG 3660  
Db 3786 GATGAAGGACGGCAATGTGGATCCAGAACTGATGATTAATAACAAAAAATCCGG 3844  
Qy 3661 GAGAAATTTGCCACTGACCGTCTTACCAATTCACACATGATGAACACCATTTATGAC 3720  
Db 3845 GAGAAATTTGCCACTGACCGTCTTACCAATTCACACATGATGAACACCATTTATGAC 3904  
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Db 3905 AGCGACAGATAATGTTTATGATTTAGATTTAGGAAAGATGATGAGCCCTATGTT 3964  
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Db 4145 TTCGAGACAGCACTGTGA 4162

## RESULT 14

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; Publication No. US20030157089A1

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; APPLICANT: Vedvick, Thomas S.  
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; APPLICANT: Wang, Aijun  
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; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C28  
; CURRENT APPLICATION NUMBER: US/10/144,678A  
; CURRENT FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 1033  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 535  
; LENGTH: 6082

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-144-678A-535  
Query Match 99.7%; Score 3966; DB 16; Length 6082;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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Qy 61 CGCGTGTCTTCTGCTGGCTCAATCCCTGTGTTAAATTTGGCCATAAACCGAGATAGAG 120  
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Qy 2941 TTGGCACTGCTTATGCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
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Qy 3001 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAAGGTCATTGAAATACACAGACTTGAA 3060  
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Qy 3121 ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGTGTAAGTGAAGAT 3180  
Db 3306 ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGTGTAAGTGAAGAT 3365

3181	QY	CTGACAGCACTCATTAATCAAGAAGAGTTGGCAATTGTGGGAAGAACCGGAGCTGGA	3240
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3541	QY	CAAGAACAACCTGGTGTGCTTGGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT	3600
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3965	DB	TTCTCTGCAAAATAAAGAGAGCCCTATTTTTACAAGATGTTGCAACAACCTGGGCAAGGCAGAA	4024
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**RESIT.T 15**

[illegible]

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Qy	1261	AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTTACTGTCAGACCTGGCGAAATG	1320
Db	1446	AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTTACTGTCAGACCTGGCGAAATG	1505
Qy	1321	TTAGCTGTGTCGCGCCGCTGGGAGCAGGAGTCATCATCTGTTAAGTGCCTGCTCGG	1380
Db	1506	TTAGCTGTGTCGCGCCGCTGGGAGCAGGAGTCATCATCTGTTAAGTGCCTGCTCGG	1565
Qy	1381	GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGATGGAAGAAATGCTATGTCTCAG	1440
Db	1566	GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGATGGAAGAAATGCTATGTCTCAG	1625
Qy	1441	CAGCCCTGGGTTCTCGGGAATCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1500
Db	1626	CAGCCCTGGGTTCTCGGGAATCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1685
Qy	1501	AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTTACAGCTGTTG	1560
Db	1686	AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTTACAGCTGTTG	1745
Qy	1561	GAGGATGGTATCTGATCTGATAGGAGATCGGGGAACCACTGAGTGAGGGGCAGAAA	1620
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Qy	1621	GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGACGAT	1680
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Qy	1681	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1740
Db	1866	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1925
Qy	1741	ATTTTGCATGAGAAAGATCACAAATTTTGTGACTCATCAGTTGCACTACCTCAAAAGTGCA	1800
Db	1926	ATTTTGCATGAGAAAGATCACAAATTTTGTGACTCATCAGTTGCACTACCTCAAAAGTGCA	1985
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Db	1986	AGTCAGATTTCTGATATTGAAAGATGGTAAATATGTTGCAGAAAGGGAATTACCTGAGTTC	2045
Qy	1861	CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA	1920
Db	2046	CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA	2105
Qy	1921	CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGCTTTGG	1980
Db	2106	CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGCTTTGG	2165
Qy	1981	TCTCAACAAATCTTACAGCCCTCTTGAAGATGGTCTCTGGAGAGCCCAAGATACAGAG	2040
Db	2166	TCTCAACAAATCTTACAGCCCTCTTGAAGATGGTCTCTGGAGAGCCCAAGATACAGAG	2225

Qy	2041	AATGTCCTCCAGTTACACTATCAGAGGAGAACCGTTTCTGAAGAAAAGTTGGTTTTTCAGGCC	2100
Db	2226	AATGTCCTCCAGTTACACTATCAGAGGAGAACCGTTTCTGAAGAAAAGTTGGTTTTTCAGGCC	2285
Qy	2101	TATAAGAAATTTACTTTACAGAGCTGGTGTCTCACTGGATTTCTTTCAATTTTCTTATTTCTCTTA	2160
Db	2286	TATAAGAAATTTACTTTACAGAGCTGGTGTCTCACTGGATTTCTTTCAATTTTCTTATTTCTCTTA	2345
Qy	2161	AACACTGACAGCTCAGGTTGCTATGTGCTTCAAGATTTGTTGGTGGCTTTCATACTGGGCAAAAC	2220
Db	2346	AACACTGACAGCTCAGGTTGCTATGTGCTTCAAGATTTGTTGGTGGCTTTCATACTGGGCAAAAC	2405
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Qy	2281	CTTAACTGGTACTTATGGAATTTTATTCAGGTTTAACTGTAGTACCGTTCCTTTTGGCATAT	2340
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Qy	2341	GCAAGATCTCTATTTGGTATTTCTAGTCTCTTGTAACTCTTCACAAAATTTTGCACAAACAA	2400
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Qy	2401	ATGTTTGAGTCAATCTGAAAGCTCCGCTATTTATTTTGTAGATAAATCCAAATAGGAAGA	2460
Db	2586	ATGTTTGAGTCAATCTGAAAGCTCCGCTATTTATTTTGTAGATAAATCCAAATAGGAAGA	2645
Qy	2461	ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTTGTCCCGCTGACGTTT	2520
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Db	2826	TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCTTGGAAATCTACAACTCGAGTFCAGATG	2885
Qy	2701	TTTTTCCACTGTGTCACTTCTCTCCAGGGGCTCTGGACCAATCCGGGATACAAAGACGAA	2760
Db	2886	TTTTTCCACTGTGTCACTTCTCTCCAGGGGCTCTGGACCAATCCGGGATACAAAGACGAA	2945
Qy	2761	GAGAGGTGTGAGAACTGTTTGTATGCAACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	2820
Db	2946	GAGAGGTGTGAGAACTGTTTGTATGCAACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	3005
Qy	2821	TTTTTGAACAGCTCCCGCTGGTTTCCCGTCCGTCTGGATGCCATCTCTGTGCCATGTTTGTG	2880
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Db	3126	TTGGCACTGTCTATATGCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3185
Qy	3001	GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATGTAATACAGACCTTGAA	3060
Db	3186	GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATGTAATACAGACCTTGAA	3245
Qy	3061	AAAGAAGCACTTTGGGAATATCAGAAACGCCACCAACAGCTGGCCCCCATGAAGGATG	3120
Db	3246	AAAGAAGCACTTTGGGAATATCAGAAACGCCACCAACAGCTGGCCCCCATGAAGGATG	3305
Qy	3121	ATAATCTTTGACAAATGTGAACCTTCAATGTAAGTCCAGGTGGGCTCTCTGGTACTGAAGCAT	3180

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Qy      3241  AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTGAGAACCCGAGGTAAATTTGGATT 3300
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Qy      3301  GATAAGATCTTGACACATGAAATTTGCACTTCAGATTAAAGGAAGAAAATGTCAATCATA 3360
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_est3.\*

4: gb\_est4.\*

5: gb\_est5.\*

6: gb\_est6.\*

7: gb\_est7.\*

8: gb\_est8.\*

9: gb\_est9.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2719.4	68.4	3685	9 AY415507	AY415507 Pan trogl
4	2289.8	57.6	3679	9 AY415508	AY415508 Mus muscu
5	1237.2	31.1	3208	3 AK032802	AK032802 Mus muscu
6	734	18.5	1084	4 BM462073	BM462073 AGENCOURT
7	725	18.2	915	5 BP382967	BP382967 BP382967
8	717.4	18.0	747	7 CF597322	CF597322 AGENCOURT
9	712.8	17.9	797	6 CD657554	CD657554 AGENCOURT
10	703.6	17.7	1679	3 CK704782	CK704782 Tetraodon
11	665.6	16.7	810	7 CF786044	CF786044 AGENCOURT
12	660.2	16.6	951	5 BU186494	BU186494 AGENCOURT
13	638	16.0	682	2 BB879353	BB879353 601484613
14	634	15.9	639	7 CN410192	CN410192 170006000
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16	620.4	15.6	1503	3 CK683466	CK683466 Tetraodon
17	614	15.4	727	2 BE879718	BE879718 601491617
18	605.8	15.2	1139	5 BQ069612	BQ069612 AGENCOURT
19	583	14.7	583	5 BP292935	BP292935 BP292935
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21	565.4	14.2	896	5 BQ889997	BQ889997 AGENCOURT
22	553.8	13.7	852	1 AJ814701	AJ814701 AJ814701
23	546	13.7	926	2 BE885514	BE885514 601508707
24	542.2	13.6	581	5 BP379624	BP379624 BP379624

25	535.6	13.5	702	6 CB451973	CB451973 706792 MA
26	521	13.1	663	7 CB452140	CB452140 706984 MA
27	502.4	12.6	761	7 CN537837	CN537837 UI-M-H50-
28	498.4	12.5	716	7 CK837582	CK837582 4062919 B
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ALIGNMENTS

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ACCESSION AY415506  
VERSION AY415506.1 GI:39771465  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 3685)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

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/gene="ABCC4"

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ORIGIN

Query Match 83.5% Score 3322.2; DB 9; Length 3685;

Best Local Similarity 90.2%; Pred. No. 0;

Matches 332; Conservative 0; Mismatches 361; Indels 0; Gaps 0;

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Db 121 GNNNNNGCCAAAGTAATCCAGGCCATATTTTGGGAAAAATTAATAATTATTTTGA AAA 180  
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Db 361 NNN 420  
Qy 606 GAACAAGTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCAGGAACACTGCAGGC 665  
Db 421 NNN 480  
Qy 666 GATCGCAGTCACTGCCCTACTCTGGATGGAGATAGGAATATCGTCCCTCTCTGGGATGGC 725  
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RESULT 2  
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 DEFINITION AK052778  
 ACCSSION AK052778.1 GI:26095372  
 VERSION HTC; CAP trapper.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishii, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)

5  
REFERENCE  
AUTHORS  
The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase 1 & II Team.  
TITLE  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL  
Nature 420, 563-573 (2002)  
REFERENCE  
AUTHORS  
6  
(bases 1 to 4594)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanganaki, T., Hara, A., Hashizume, M.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
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Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
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URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216]  
COMMENT  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
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FASTY, 86.9%ID, 98.1%length, match=3904)"  
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Best Local Similarity 81.5%; Pred. No. 0;  
Matches 3185; Conservative 0; Mismatches 721; Indels 1; Gaps 1;  
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Qy 1333 GGCCCCGTGGGACAGGGAAGTCACTCACTTAAAGTCCGCTGCGGGGAATTTGGCCCCA 1392  
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Db	2446	CTGGTGTTCTATATCTCTGTGAACGCTTCCAGACTTTTGACAACTTTTGAGTGCC	2505
Qy	2413	ATTCTGAAAGCTCCGGTATTTATCTTTGATAGAAATCCAAATAGGAAGAAATTTTAAATCGT	2472
Db	2506	ATACTGAAGGCTCCGGTGTGTTCTTCGACAGAAATCCAAATCGGGAGGATTTTAAATCGT	2565
Qy	2473	TTCTCCAAAGACATTTGACACTTGGATGATTTGTCGCGCTGACGTTTGTAGATTTTCAATC	2532
Db	2566	TTCTCCAAAGACATTCGACACATGATGATTTGTTCTTCCCTGACGTTTCTTGGACTTCATC	2625
Qy	2533	CAGACATTTGCTACAAGTGGTGGTCTCTGTGGCTGTGGCCGTGATTTCTTGGATC	2592
Db	2626	CAGAGCTTGCTCCTCGTCTGTAAGTGTGATCGCTGTGGCCGCGGTGATCCTTGGATC	2685
Qy	2593	GCAATACCTTTGGTTCCTCTGGAAATCATTTTCAATTTTCTTCGCGGAAATTTTGTGAA	2652
Db	2686	CTCATACATTTGGTTCGCTCTCAGTCTGTCTTCTCGGTCTTCTCGGAGATCTTCTTAGAG	2745
Qy	2653	ACGTCAAGAGATGTGAAGCGCTCGAATCTACAACTCGAGTCCAGTGTGTTTCTCCACTTG	2712
Db	2746	ACGTCAAGGATGTCAAGCGCTGGAATTCACAAACGAGGCCGCTTATTTCTCCATTTA	2805
Qy	2713	TCATCTTCTCTCCAGGGGCTCTGACCATTCGGGCATACAAAGCAGAGAGGAGTGTGAG	2772
Db	2806	TCGTCTCTCTCCAGGGGACTCTGGACCATTCGGGCATTCACAAAGCTGAGGAGAGTGTGAG	2865
Qy	2773	GAACTGTTGATGACACACAGGATTTACATTTACAGAGGCTTGGTCTTGTGTTTTCACAAAG	2832
Db	2866	GAGCTGTTGATGACACACAGGACTTGCATTTACAGAGGCTTGGTCTTGTGTTTTCACAAAG	2925
Qy	2833	TCCGCTGG--TTGCGCGTCTGATGATGCACTGTGCGCATGTTTGTTCATCATCTGTTGC	2891
Db	2926	TCGAGATGGTTTCTGTGCTCTGAGCGCATCTGCGCATCTTTGTAATCTGTCGTTGC	2985
Qy	2892	CTTTGGGTCTCTGATTTCTGCAAAACTCTGGAATGCGGGCAGGTTGGTTTGGCACTGTC	2951
Db	2986	CTTCGGGTCTCTGTTCTGCGGAAGACTTTGAAATGCTGGCAGGTTGGCTTGGCTTGTGTC	3045
Qy	2952	CTATGCTCTCAGCTCATGCGGATGTTTCAAGTGTGTGTCGACAAAGTGTCTGAAGTTGA	3011
Db	3046	CTACGCTCTCACACTCATGCGGATGTTTCCAGTGTGTCGACAGAGCGCGGAAGTAGA	3105
Qy	3012	GAATATGATCATCTCAGTAGAAGGGTCAATTGAAATACAGAGCTTGAAGAGAGCACC	3071
Db	3106	GAATATGATCATTTTCAAGTGTGAGAGAGTGTGAGTACACGAGCTTAGAGAGAGGCGCC	3165
Qy	3072	TTGGGAATATCAGAAACGCCACCCAGCTTGCGCCCATGAAGAGTGTAACTTTTGA	3131
Db	3166	TTGGGAGTCAAGNAGGCCCAACCCAGCTTGCGCCCAAGAGGAGTCTATCTGTTTGA	3225
Qy	3132	CAATGTGAACTTCAATGTACAGTCAAGTGGGCTCTGCTACTGAAGCATCTGACAGCACT	3191
Db	3226	CAATGTGAACTTCACTTACAGCTTAGATGGGCTCTGCTTCTGAAGCACCCTGATGCGCT	3285
Qy	3192	CATTAAATCAGAGAAAGGTTGCAATTGCGGAGAACCGGAGCTCGGAAAGTTCCT	3251
Db	3286	CATCAAGTCCAGGAAAGGTTGGAATTTGCGGAGAACCGGAGCTGGGAAAGCTCCCT	3345
Qy	3252	CATCTCAGCCCTTTTATGATTTGTCAGAAACCGAGGTAAATTTGGATTTGATAGATCTT	3311
Db	3346	CATCTCGGCTCTTTCAGGCTGTACAGAACCGAGGGGAAATCTGGATCGATAGATCTT	3405
Qy	3312	GACAACTGAAATTTGAGCTTCAAGTTTAAAGAAAGAAATGTCAATCATCTCAGGAAAC	3371
Db	3406	GACAAACGAAATTTGGGCTTCAAGCTTAAAGAAAGAAATGTCAATCATCAGGAAAC	3465
Qy	3372	TGTTTGTGCTCAGTGAACATGAGGAAACCTGGATCCCTTTTAAAGAGCAGACGGATGA	3431
Db	3466	TGTTTGTGCTCAGTGAACATGAGGAAACCTGGATCCCTTTTAAAGAGCAGACGGATGA	3525
Qy	3432	GGAACTGTGAAATGCTTACAGAGGTACAACTTAAAGAAACCAATTTGAAGATCTTCTCGG	3491
Db	3526	GGAGCTGTGAGGGGCTTTGAGGAGGTACAACTTAAAGAGGCCATTTGAAGATCTTCTCGG	3585
Qy	3492	TAAAAATGGAATCTGAAATTTAGCAGAACTCAGGATCCAAATTTTGTGTTGGACAAAGCAACT	3551
Db	3586	AAAAATGGAATCTGAAATTTAGCAGAACTCAGGATCCAAATTTTGTGTTGGACAGAGACAGT	3645
Qy	3552	GGTGTGCTTGGCAGGGCAATTTCTCAGGAAATCAGATTTGATTTGATTTGATGAGGAC	3611
Db	3646	AGTGTGCTTGGCAGGGCCATTTCTAAAGAAATAACCGAATACTGATCATTTGATGAGCAAC	3705





Qy	1266	ATCAGAGACCCCAACTCTACAAAGCCCTTTCCTTACTGTCTAGACTGGCGAATTGTTAGC	1325
Db	1081	ATCAGAGACCCCAACTCTACAAAGCCCTTTCCTTACTGTCTAGACTGGCGAATTGTTAGC	1140
Qy	1326	TGTGGTCGGCCCGTGGAGCAGGAGTCACTGTTAAGTCCGTCGCGGAATT	1385
Db	1141	TGTGGTCGGCCCGTGGAGCAGGAGTCACTGTTAAGTCCGTCGCGGAATT	1200
Qy	1386	GGCCCCAAGTCAAGCGCTGGTCAGCGTGCATGGAAGAAATGCCCTATGTCTCAGCAGCC	1445
Db	1201	GGCCCCAAGTCAAGCGCTGGTCAGCGTGCATGGAAGAAATGCCCTATGTCTCAGCAGCC	1260
Qy	1446	CTGGGTGTTCTCGGAACTCTGAGAGTAATATTATTTTCGGGAAGAAATACGAAAAGGA	1505
Db	1261	CTGGGTGTTCTCGGAACTCTGAGAGTAATATTATTTTCGGGAAGAAATACGAAAAGGA	1320
Qy	1506	ACGATATGAAAAGTCAATAAGGCTTGTCTCTGAAAAGAAATTTACAGCTGTTGGAGGA	1565
Db	1321	ACGATATGAAAAGTCAATAAGGCTTGTCTCTGAAAAGAAATTTACAGCTGTTGGAGGA	1380
Qy	1566	TGGTGATCTGACTGTGATAGGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAAGCAGC	1625
Db	1381	NN	1440
Qy	1626	GGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGATCTCT	1685
Db	1441	NN	1500
Qy	1686	CAGTGCAGTAGATCGGAGTTAGCAGACACTTGTTCGAACGTGTATTGTCAAATTTT	1745
Db	1501	CAGTGNNNNNNTCGGAAGTTAGCAGACACTTGTTCGAACGTGTATTGTCAAACCTTT	1560
Qy	1746	GCATGAGAAGATCAAAATTTTAGTGACTCATCAGTTGCAAGTCTCAAAGCTGCAAGTCA	1805
Db	1561	GCATGAGAAGATCAAAATTTTAGTGACTCATCAGTTGCAAGTCTCAAAGCTGCAAGTCA	1620
Qy	1806	GATTCTGATATTGAAAGATGTAATAATGGTCAGAAAGGGACTTACACTGATGTTCTTAAA	1865
Db	1621	GATTCTGATATTGAAAGATGTAATAATGGTCAGAAAGGGACTTACACTGATGTTCTTAAA	1680
Qy	1866	ATCTGGTATAGATTTGGCTCCCTTTTAAAGAGGATAATGAGAAAGTGAACACCTCC	1925
Db	1681	ATCTGGTATAGATTTGGCTCCCTTTTAAAGAGGATAATGAGAAAGTGAACACCTCC	1740
Qy	1926	AGTTCCAGGAATCCCACTAAGAAATCGPACCTTCTCAGAGTCTTCGGTTGGTCTCA	1985
Db	1741	AGTTCCAGGAATCCCACTAAGAAATCGPACCTTCTCAGAGTCTTCGGTTGGTCTCA	1800
Qy	1986	ACAACTTCTAGACCTCTCTTGAAGATGGTGTCTCTGGAGGCCAAGATACAGAGAATGT	2045
Db	1801	ACAACTTCTAGACCTCTCTTGAAGATGGTGTCTCTGGAGGCCAAGATACAGAGAATGT	1860
Qy	2046	CCCAAGTTACTATCAGAGGAAACCGTTCTGAAAGAAAAGTTGGTTTTAGGGCTATAA	2105
Db	1861	CCCAAGTTACTATCAGAGGAAACCGTTCTGAAAGAAAAGTTGGTTTTAGGGCTATAA	1920
Qy	2106	GAATTAATTCAGAGCTGTGCTCACTGATGTCTTCAATTTTCTTATTTCTCTTAAACAC	2165
Db	1921	GAATTAATTCAGAGCTGTGCTCACTGATGTCTTCAATTTTCTTATTTCTCTTAAACAC	1980
Qy	2166	TGCAGCTCAGGTGCCCTATGTCTCAAGATTTGGTGGCTTTTATATCTGGGCAAAACAAAC	2225
Db	1981	TGCAGCTCAGGTGCCCTATGTCTCAAGATTTGGTGGCTTTTATATCTGGGCAAAACAAAC	2040
Qy	2226	AAGTATGCTAAATGCTGTAATGAGGAGGAAATGTAAACCGAAGCTAGATCTTTAA	2285
Db	2041	AAGTATGCTAAATGCTGTAATGAGGAGGAAATGTAAACCGAAGCTAGATCTTTAA	2100
Qy	2286	CTGGTACTTAGGAATTTATTACAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAG	2345
Db	2101	CTGGTACTTAGGAATTTATTACAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAG	2160
Qy	2346	ATCTCTATTGGTATTCTACGCTCTTGTAACTCTTTCACAACTTTGCAACAAATGTT	2405

Db	2161	ATCTCTATTGGTATTCTACGCTCTTGTAACTCTTTCACAACTTTGCAACAAATGTT	2220
Qy	2406	TGAGTCAATTTCTGAAAGCTCCGGTATTATTCTTTGTAGTAAGAAATCCAATAGGAAGATTTT	2465
Db	2221	TGAGTCAATTTCTGAAAGCTCCGGTATTATTCTTTGTAGTAAGAAATCCAATAGGAAGATTTT	2280
Qy	2466	AAATCGTTTTCTCCAAAGACATTTGACACTTTGGATGATTTGCTGCGCTGACGTTTTAGA	2525
Db	2281	AAATCGTTTTCTCCAAAGACATTTGACACTTTGGATGATTTGCTGCGCTGACGTTTTAGA	2340
Qy	2526	TTTCATCCAGACATTTGCTACAAGTGGTGGTGTGGTCTCTGTGGCTGTGGCCGATTTCC	2585
Db	2341	TTTCATCCAGNNNTTGTCTACAAGTGGTGGTGTGGTCTCTGTGGCTGTGGCCGATTTCC	2400
Qy	2586	TTGGATCGCAATACCCCTTGGTTCCTTGGAACTCAATTTTCAATTTTCTTCCGCCGATATT	2645
Db	2401	TTGGATCGCAATACCCCTTGGTTCCTTGGAACTCAATTTTCAATTTTCTTCCGCCGATATT	2460
Qy	2646	TTTGGAAACGTCAGAGATGTGAAGCGCTTGGAACTCTAACCTCGGAGTCCAGTGTTTTC	2705
Db	2461	TTTGGAAACGTCAGAGATGTGAAGCGCTTGGAACTCTAACCTCGGAGTCCAGTGTTTTC	2520
Qy	2706	CCACTTGTCTATTTCTCTCCAGGGGCTCTGGAACCATCCGGGCATACAAAGCAGAAGAG	2765
Db	2521	CCACTTATCATCTTCTCTCCAGGGGCTCTGGAACCATCCGGGCATACAAAGCAGAAGAG	2580
Qy	2766	GTGTCCAGGAACGTTTTCATGCACACAGGATTTACATTTACAGAGCTTGGTTCGTTTTT	2825
Db	2581	GTGTCCAGGAACGTTTTCATGCACACAGGATTTACATTTACAGAGCTTGGTTCGTTTTT	2640
Qy	2826	GACAACTCCCGCTGGTTCGCGCTCTGGATGCCATCTGTGCCATGTTTGTTCATCAT	2885
Db	2641	GACAACTCCCGCTGGTTCGCGCTCTGGATGCCATCTGTGCCATGTTTGTTCATCAT	2700
Qy	2886	CGTTGCCCTTTGGGTCCCTGATTTCTGGCAAAAATCTCTGGATGCCGGGAGGTTGGTTGGC	2945
Db	2701	CGTTGCCCTTTGGGTCCCTGATTTCTGGCAAAAATCTCTGGATGCCGGGAGGTTGGTTGGC	2760
Qy	2946	ACTGTCTATGCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTCTCGACAAAGTCTGA	3005
Db	2761	ACTGTCTATGCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTCTCGACAAAGTCTGA	2820
Qy	3006	AGTTGAGAATATGATGATCTCAGTAGAAAAGGTCATTTGAATACACAGACCTTTGAAAAA	3065
Db	2821	AGTTGAGAATATGATGATCTCAGTAGAAAAGGTCATTTGAATACACAGACCTTTGAAAAA	2880
Qy	3066	AGCACTTTGGGAATATCAGAAAACGCCCAACCGGCTGGCCCCATGAAAGGATGATAAT	3125
Db	2881	AGCACTTTGGGAATATCAGAAAACGCCCAACCGGCTGGCCCCATGAAAGGATGATAAT	2940
Qy	3126	CTTTGCAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAGCATCTGAC	3185
Db	2941	CTTTGCAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAGCATCTGAC	3000
Qy	3186	AGCACTCATTTAAATACAAAGAAAAGTTGGCATTTGGGAAGAACCGGAGCTGAAAAAG	3245
Db	3001	AGCACTCATTTAAATACAAAGAAAAGTTGGCATTTGGGAAGAACCGGAGCTGAAAAAG	3060
Qy	3246	TTCCCTCATCTCAGCCCTTTTATGATTTGT CAGAAACCCGAAAGGTAAAAATTTGGATTTGATAA	3305
Db	3061	NN	3120
Qy	3306	GATCTTGACAACTGAAATTTGGACTTCAGGATTTAAGGAAGAAATGTCAATCATACCTCA	3365
Db	3121	NN	3180
Qy	3366	GGAACTGTTTTGTTTCACTGAAACAAATGAGAAAAACCTGGATCCCTTTTAAATGAGCACAC	3425
Db	3181	NGAACCTGTTTTGTTTCACTGAAACAAATGAGAAAAACCTGGATCCCTTTTAAATGAGCACAC	3240
Qy	3426	GGATGAGGAATCTGTGGAACTCCCTTACAGAGGTACAACTTTAAAGAAACCAATTTGAAGATCT	3485



Db 1016 ACCATCTGATGGCAAGCCATTGTCCACGTGCAAGATTTCACCGCTTCTCGGCAAGGC 1075  
Qy 1266 ATCAGAGACCCCAACTCTCAAGGCTTTCTCTTACTGTCAAGCTCGCGAATTTGTAGC 1325  
Db 1076 ACTAGACAGTCCAACTCTGCAAGGTCTTCTTTATTGCCAGACTGCTGAGTTGTTAGC 1135  
Qy 1326 TGTGCTCGGCCCGTGGAGCAGGGAAGTCACTGTTAAAGTGCCTGCTCGGGGAATT 1385  
Db 1136 CGTGGTTGGCCCACTTGGAGCAGGCAAGTCTGCTGTGAGCGCAGTCTGGGTGAGCT 1195  
Qy 1386 GGGCCCAAGTCAAGGCTGCTCAGCTGCAAGGAAGTTCCTATGCTCTCAGCAGCC 1445  
Db 1196 GCTTCTCGCAGCGGCTGCTCAGCTGCAAGGAGGATCGCTTCTCAGCAGCC 1255  
Qy 1446 CTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTATTTTCGGGAAGAAATACGAAAGGA 1505  
Db 1256 CTGGGTGTTCTCGGCACTGAGGAGCAATATTATTTGGGAAGAAATATGAGAAGGA 1315  
Qy 1506 ACGATATGAAGAAAGTCAAAAGGCTGTGCTCTGAAAGGAATTTACAGCTGTTGGAGGA 1565  
Db 1316 GCGATATGAGAAAGTGAATCAAGGCTGTGCTCTGAAGAAAGACCTGCAAGCTTCTGGAGGA 1375  
Qy 1566 TGGTATCTGACTGTGATAGAGATCGGGGAACCAAGCTGAGTGGAGGCGAAGAACAG 1625  
Db 1376 CGGGGATCTGACGGTATAGAGAGACCGGGGAGCCACGCTGAGTGGAGGCCAGAAAGCTCG 1435  
Qy 1626 GGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAACGATCTCT 1685  
Db 1436 GGTGAACTGTGCAAGGCGGCTGTACAGGAGCGCGACATCTACCTCTTGTATGATCGCT 1495  
Qy 1686 CAGTGCAGTATGATCGGAAGTTAGCAGACACTTGTTCGAACTGTGTTATTTGTCAAAATTTT 1745  
Db 1496 CAGGCTGTGATGCAAGTGGGCAAGCACCTGTCTCAACTGTGTATCTGTCAAGGCGTT 1555  
Qy 1746 GCATGAGAGATCAAAATTTAGTGAATCATCAGTTCAGTACCTCAAGCTGCAAGTCA 1805  
Db 1556 GCACGAGAGATCAAAATTTAGTGAATCATCAGTTCAGTACCTCAAGCTGCAAGCCTCA 1615  
Qy 1806 GATTCTGATATTGAAGATGTAATAATGTCAGAGGGGACTTTACACTGATGTTCTTAAA 1865  
Db 1616 CATCTCATCTAAAGATGAGATGTTGTCAGAGGGGACTTTACAGGGGACTTTACAGGGATTTCTGAA 1675  
Qy 1866 ATCTGGTATGATTTGGCTCCCTTTTAAAGAGGATAAAGAGAAAGTGAACAACTCC 1925  
Db 1676 ATCTGGTGTAGATTTGGCTCCCTGTTTAAAGAAAGAAACAGGAAAGCAGAGCCCTCCAC 1735  
Qy 1926 AGTTCAGGAATCCCACTAAGGAATCGTACCTCTCAGAGTCTTCGGTTTGGTCTCA 1985  
Db 1736 AGCCCCAGGAACCCCGACCTCAGGAACCGAACCTTCTCGAGGCTCAATTTTGGTCTCA 1795  
Qy 1986 ACAATCTCTAGACCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGT 2045  
Db 1796 GCAGTCACTCAGACCTCTGTTTGAAGAGCGGGGCCCAAGAGGCCAAGCAGAGAGAAC 1855  
Qy 2046 CCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAGTGGTTTTTCAGGCTTATAA 2105  
Db 1856 GCAGCAGTGCACCCGAGGAGAGCCGTTCCGAAGGGAGATCGCTTCAAGGCCCTACAA 1915  
Qy 2106 GAATTAATCTCAGAGCTGGGTCTCACTGGAATGCTTCAATTTCTTATTTCTCTTAAACAC 2165  
Db 1916 GAATTAATCTCTCGGCGGCGCATCTCTGTTCTTCAATTTCTCTGCTGTCTTAAACAT 1975  
Qy 2166 TGCAGCTCAGTTCCTATGCTTCAAGATGGTGGCTTTCATCTGCGCAACAAACA 2225  
Db 1976 GGTGGCCAGGTTTCTATGTTCTTCAAGGACTGGTGGCTTTCACCTGCGGCAACAGCA 2035  
Qy 2226 AAGTATCTCTAAATGCTGCTGTAATGGAGGAGGAATGTAAACGAGAGCTTAGATCTTAA 2285  
Db 2036 AGGTGCACTGACAAACCAAGAAATCGAATGGAATATTAACGGAGACCCTTAGACCTCAG 2095  
Qy 2286 CTGCTACTAGGAATTTATCAGGTTTAACTGATAGCTACCGCTTCTTTTGGCATAGCAAG 2345  
Db 2096 CTGCTACTAGGAATTTACGAGGTCTAACTGCGGTCAACGCTCTCTTTTGGCATAGCGAG 2155

Qy 2346 ATCTCTATTTGGTATTTCTACGTCCTTTGTAACTCTTCAAACTTTTGACAAACAAATGTT 2405  
Db 2156 ATCCCTACTGGTGTCTTATATCTTTGAAAGCTTCCAGACTTTTGACAAACAGATGTT 2215  
Qy 2406 TGAGTCAATTTCTGAAAGCTCGGTATTTATTTCTTTGATAGAAATCAATAGGAAGATTTT 2465  
Db 2216 TGAGTCCATACTGAAAGCTCCCGTGTGTTGTTCTTTTGACAGAAATCAATCGGAGGATTTT 2275  
Qy 2466 AAATCGTTTTCTCAAAGACATTTGACACTTTGGATTTGCTGCGCTGAGCTTTTATA 2525  
Db 2276 AAATCGTTTTCTCAAAGACATTTGACACTTTGGATTTGCTGCGCTGAGCTTTTATA 2335  
Qy 2526 TTTTCATCCAGACATTTGCTACAGTGGTGTGCTCTCTGTGGCTGTGGCCGCTGATTC 2585  
Db 2336 CTTTCATCCAGAGCTTGTCTCTCGTGAAGTGTGATCGCTGTGGCCGCGGCTGATCCC 2395  
Qy 2586 TTGATCGCAATACCTTTGGTTCCTTCCCTTGGATCATTTTTCATTTTCTTCCGCGATATT 2645  
Db 2396 TTGATCTCTCATACCATTTGGTTCGCTCTCAGTCTCTTCTGCTGTTCTTCCGAGATACTT 2455  
Qy 2646 TTTGGAAACCTCAAGATGTTGAAGCGCTTGAATCTACACTCGGAGTCCAGTGTTC 2705  
Db 2456 CTTAGAGACCTCAGGGATGTCAAGCGCTTGAATTCAC - ACACGGAGCCCGTATTCTC 2514  
Qy 2706 CCACTTGTCTCTCTCTCCAGGGCTCTTGACCATCCGGGCATACAAAGCAGAGAGAG 2765  
Db 2515 CCATTTATCGTCTCTCTCCAGGACTCTGGACCATCGGGCTTACAAAGCTGAGGAGAG 2574  
Qy 2766 GTGTCAGAACTGTTTGTATGCACACAGGATTTATTCATTCAGAGCTTGGTTCCTGTTTTT 2825  
Db 2575 GTGTCAGAGCTGTTTGTATGCACACAGGACTTGTCAATTCAGAGCTTGGTTCCTGTTCT 2634  
Qy 2826 GACAACTCCGCTGGTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2885  
Db 2635 GAGACATCAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2694  
Qy 2886 CGTTCCTTTGGGTCCCTGATTTCTGGCAAAACCTCTGGATGCCGGGAGGTTGCTGTTGGC 2945  
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Qy 2946 ACTGCTCTATGCTCTCAAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005  
Db 2755 CTTGCTCTAGCTCTCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2814  
Qy 3006 AGTTGAAATATGATGATCTCAGTGAAGAGGCTTGAATATACACAGACCTTGAAGAA 3065  
Db 2815 AGTAGAATATGATGATTTTCACTGAGAGAGTGAATGAGTACACGACCTTAGAGAAGGA 2874  
Qy 3066 AGCACTTTGGGAATATCAGAAACGCCCAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3125  
Db 2875 GGGCTTTGGAGTGCAGAAAGCGCCCAACCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2934  
Qy 3126 CTTTGAATATGAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3185  
Db 2935 CTTTGAATATGAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2994  
Qy 3186 AGCACTTAAATATCAAGAAAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3245  
Db 2995 TGGCTCATCAAGTCCAGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3054  
Qy 3246 TTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3305  
Db 3055 NNN 3114  
Qy 3306 GATCTTTGACAACTGAAATTTGACATTCACGATTTAAAGGAAGAAATGTCATACCTCA 3365  
Db 3115 NNN 3174  
Qy 3366 GGAACCTGTTTGTTCATGAGAAACCACTGAGTCCCTTTTAAATGAGACAC 3425  
Db 3175 NGAACCTGTTTGTTCATGAGAAACCACTGAGTCCCTTTTAAATGAGACAC 3234

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Qy 3426 GGATGAGGAACGTGGGAATGCTTCAAGAGGTCAACCTTAAAGAAACCATTGAAGATCT 3485
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Db 3235 GGACGAGAGCTGTGGAGGCTTGGAGAGGTAACTTAAAGAGCCATTGAAGATCT 3294
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Qy 3486 TCCTGGTAAATAGGATAGTAAATAGCAGATCAGGATCCAAATTTTAGTGTGGACAAAG 3545
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Db 3295 TCCTGGAAATAGTAAATAGCAGATCAGGATCCAAATTTAGTGTGGACAGAG 3354
|||
Qy 3546 ACACTGGTGGCTTGGCAGGCAATCTCAGAAAAATCAGATATGATTATGATGA 3605
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Db 3355 ACAGTATGTGGCTTGCAGGGCCATTTAAAGAATAACCGAATCTGATCATTTGATGA 3414
|||
Qy 3606 AGGCACGCGCAATGTGATCAAGCACTGATGAGTTAATACAAAAAATCCGGGAGAA 3665
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Db 3415 AGCAACTGCAATGTGACCCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3474
|||
Qy 3666 ATTTGCCCACTGCACCGCTGTCAACATTGCACACAGATGAACACCATTTATTCAGCGGA 3725
|||
Db 3475 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3534
|||
Qy 3726 CAAGATATGTTTATGATTCAGGAAGCTGAAGAATATGATGAGCGGTATGTTTGTCT 3785
|||
Db 3535 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3594
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Qy 3786 GCAAAATAAAGAGAGCGCTATTTTCAAGATGTCGCAACACTGGCGCAGGAGCGCGC 3845
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Db 3595 GCAGATCCAGAGAGCGCTCTTTTCAAGATGTTTCAGCAACTGGCGCAGGAGCGCGC 3654
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Qy 3846 TGCCTCTCACTGAACAGCAAAACAG 3870
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Db 3655 TGCCCTCACCAGAAACAGCAAAACAG 3679
|||

RESULT 5
AK032802
LOCUS
DEFINITION Mus musculus 12 days embryo male wolffian duct includes surrounding
region cDNA, RIKEN full-length enriched library, clone:6720455A17
product:ATP-binding cassette, sub-family C (CFTR/MRP), member 4
homolog (Human), full insert sequence.
ACCESSION AK032802
VERSION AK032802.1 GI:26083045
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
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11076861
4
REFERENCE The RIKEN Genome Exploration Research Group Phase II Team and the
AUTHORS FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE
AUTHORS
5
TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
JOURNAL Group Phase I & II Team.
AUTHORS Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE
AUTHORS
6 (bases 1 to 3208)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, K., Saito, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
FEATURES
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Matches 1392; Conservative 0; Mismatches 258; Indels 0; Gaps 0;
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 18.5%; Score 734; DB 4; Length 1084;

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Qy 2123 GTGCTCACTGGAATGCTTCTCATTTTCTTAATCTTCTTAACACCTGACGCTCAGGTTCCCT 2182  
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Qy 2183 ATGTGCTTCAAGATGCTGCTTCTTCACTATGCGGCAACAAACAAAGATGCTAAATGCTCA 2242  
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Qy 2363 ACGTCTTGTAACTCTTCAAACTTTTGCAACAAATGTTTGAAGTCAATTTCTGAAAG 2422  
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Qy 2423 CTCGGTATTATTTCTTGTAGTAAATCCATAGGAAGTAAATTTAAATCGTTTCTCCAAAG 2482  
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Qy 2603 TGGTTCCTTGGAACTTCAATTTCTTTCGGCGATATTTTTCGAAACGTCAGAG 2662  
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Qy 2663 ATGTGAAGCGCTGGAATCTACAACTCGGAGTCCAGTGTTCCTTTCATCTTCTC 2722  
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Qy 2723 TCCAGGGCTCTCG 2736  
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DEFINITION BP382967 Sugano cDNA library, ilea mucosa Homo sapiens cDNA clone  
kai1118, mRNA sequence.  
ACCESSION BP382967  
VERSION BP382967.1 GI:52419393  
KEYWORDS EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 915)  
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,  
Mizushima-Sugano,J., Nakai,K. and Sugano,S.  
Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp.

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Matches 750; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Qy 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 2340  
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Qy 2341 GCAAGATCTCTATTTGGTATTTCTACGTCCTTGTAACTTTTCAAAAATTTTGCACAA 2400  
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Qy 2401 ATGTTTGAAGTCAATTTGAAAGCTCCGGTATTTATTTCTTATAGTAATCAATAGGAAGA 2460  
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Qy 2521 TTAGATTTTCAACAGACATTTGTACAGTGGTGGTGGTGGTCTCTGTGGCTGTGGCGCTG 2580  
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Qy 2641 TATTTTGTGAACGCTCAAGAGATGTGAAGCGCTGGAATCTACAACTCCGAGTCCAGTG 2700  
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Qy 2821 TTTTGTGAACAGTCCCGCTGTTTCCGCTCCGCTCTGTGATGCCATCTCTGTGCATCTTTGTC 2880  
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Qy 2881 ATCATCGTCCCTTTGGGTCCCTGATTTCTGGCAAAAATCTCTGGATGCCGGGAGGTTGGT 2940  
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/notes="vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199] from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from Wicell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6 cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with Trizol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID: 11544199] Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCGATCGAGCGCGCTTTT-3'] from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

## ORIGIN

Query Match 17.9%; Score 712.8; DB 6; Length 797;  
Best Local Similarity 99.6%; Pred. No. 1.2e-191;  
Matches 725; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 431 GCGCAATTGTTAGCTGTGTCGCGCCCGTGGAGCAGGGAAGTCATCACTGTTAAGTGCC 490  
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DEFINITION Tetraodon nigroviridis full-length cDNA.  
ACCESSION CR704782  
VERSION CR704782.1 GI:51202691  
KEYWORDS HTC; cDNA; full-length; Tetraodon nigroviridis.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 1679)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -  
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
The sequences are based on single pass reads.  
More information available at  
http://www.genoscope.cns.fr/tetraodon.  
FEATURES  
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Qy 3800 GCCTATTTTCAAGATGGTGCACAACTGGCAAGCAGAGAGCGCTCCCTCTACTGAAA 3859  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 810)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cga@nci.nih.gov  
 Tissue Procurement: James Martin, University of Iowa  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
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 http://image.llnl.gov  
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 cloned. Denatured RNA was size fractionated on a 1% agarose  
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 primer containing a Not I site. Double strand cDNA was  
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 EcoR I adaptor, digested with Not I and then cloned  
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 4-5kb. Adaptors 5'(AATTCGGCAGG)3' and 5'd  
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 Sequencing primers 3'end: T3 promoter primer 5'd  
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 (TAATACGACTCATAGG)3'. Library was constructed in the  
 laboratory of M. Bento Soares. Note: this is a NIH\_MGC  
 Library"

ORIGIN

Query Match 16.7%; Score 665.6; DB 7; Length 810;  
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 Qy 8 CCAAGATTCCTGAGAGTTCCTGCTCAGGGGAGTGAATTTGGCTTCATTTTTTCAGTGCAA 67  
 Db |||||  
 Qy 983 GCAAAATCATCGTGTGTCACCTTACCACCTACGTGCTCTCGGAGTGATGATCAG 1042  
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Db 68 GCAAAATCATCGTGTGTTGTGACCTTACACACCTACGTGCTCCTCGGAGTGTGATCACAG 127  
Qy 1043 CCAGCCGCGTGTGCGTGGCAGTGACGCTGATGCGGCTGTGCGGCTGACGGTTACCCCTCT 1102  
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VERSION BUI86494.1 GI:22700478  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 951)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Straubeberg, Ph.D.  
Email: csapb@remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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Location/Qualifiers  
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RESULT 13  
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Average insert size 2.5 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 16.6%; Score 660.2; DB 5; Length 951;  
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Qy 279 AGTTTTGGGAATTTTACGTTAAATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTT- 337  
Db 61 AGTTTTGGGAATTTTACGTTAAATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTN 120  
Qy 338 TGGGAAAAATTAATTAATTTTGAATAATATGATCCATGGATTCGTGGCTTTGAACA 397  
Db 121 TGGGAAAAATTAATTAATTTTGAATAATATGATCCATGGATTCGTGGCTTTGAACA 180  
Qy 398 CAGCTACGCTATGCCCAGCTGCTACTTTTTCAGCGCTCATTTTGGCTTACTGTCATC 457  
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Qy 458 ACTTATATTTTATCAGCTTCACTGTCTCGGATAGGTTACAGTAGCAGCATGFGCCATA 517  
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Qy 578 AGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTAC 637  
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Qy	1826	GTAATAATGTTGCAGAAAGGGGACTTACACTGAGTTCCTAAAAATCTGGTATAGATTTTGGCT	1885		
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VERSION	CN410192.1	GI:47397316			
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ORGANISM	Homo sapiens				
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1 (bases 1 to 639)				
	Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,				
AUTHORS	Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,				
	Lebkowski,J and Stanton,J.W.				
	Transcriptome characterization elucidates signaling networks that				
	control human ES cell growth and differentiation				
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)				
	Contact: Brandenberger R				
	Regenerative Medicine				
	Geron Corporation				
COMMENT	230 Constitution Drive, Menlo Park, CA 94025, USA				
	Tel: 650 473 8658				
	Fax: 650 473 7760				
	Email: rbrandenberger@geron.com				
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ACCESSION CK776984
VERSION CK776984.1 GI:42731404
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SOURCE Bos taurus (cow)
ORGANISM Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 865)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Caeas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
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FEATURES
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Best Local Similarity 83.0%; Pred. No. 3.4e-165;
Matches 719; Conservative 0; Mismatches 146; Indels 1; Gaps 1;
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Db 26 TCCGGGTAGATTTTGCTTCCCTTTT 1

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Job time : 12067 secs

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3	366	9.2	486	9	HSUB3660	U83660 Human multi
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C 5	308	7.7	407	6	CQ508484	CQ508484 Sequence
6	283	7.1	442	6	CQ492361	CQ492361 Sequence
7	260	6.5	443	6	AR562517	AR562517 Sequence
8	252	6.3	425	6	CQ510062	CQ510062 Sequence
9	250	6.3	250	6	AX046491	AX046491 Sequence
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11	216	5.4	291	6	AR405803	AR405803 Sequence
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13	216	5.4	291	6	AX201050	AX201050 Sequence
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18	208	5.2	482	6	CQ479608	CQ479608 Sequence
19	196	4.9	456	6	CQ489549	CQ489549 Sequence

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Qy 3762 ATATGATGAGCGGTATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTACAGATGGTGCA 3821

Db 301 ATATGATGAGCGGTATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTACAGATGGTGCA 360

Qy 3822 ACAACTGGCGAAGCAGAACCGCTGCCCTCACTGAAACAGCAAAAACAGGTATATCTCAA 3881

Db 361 ACAACTGGCGAAGCAGAACCGCTGCCCTCACTGAAACAGCAAAAACAGGTATATCTCAA 420

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Qy 3942 GCCCTCGACCTTAACTATTT 3961

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RESULT 2

LOCUS A64694

DEFINITION Sequence 60 from Patent WO9731111.

ACCESSION A64694

VERSION A64694.1 GI:4530759

KEYWORDS

SOURCE

ORGANISM

unidentified

unclassified.

REFERENCE 1

AUTHORS Oude, E.R., Paulusma, C.C., Bosma, P.J., Borst, P., Evers, R., Kool and Marcel.

TITLE A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM

JOURNAL Patent: WO 973111-A 60 28-AUG-1997;

COMMENT INTRIGENE BV (NL)

Other publication AU 1736697 19970910.

FEATURES

source

1..486

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ORIGIN

Query Match 9.2%; Score 366; DB 6; Length 486;

Best Local Similarity 100.0%; Pred. No. 3.2e-196;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3462 ACTTAAAGAAACCATTTGAAGATCTTCTCGTAAATGATGACTCAATTTAGCAGATCAGG 3521

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Qy 3522 ATCCAAATTTAGTGTGTCGACAAAGACAACTGGTGTGCTTGCCAGGGCAATTTCTCAGAA 3581

Db 61 ATCCAAATTTAGTGTGTCGACAAAGACAACTGGTGTGCTTGCCAGGGCAATTTCTCAGAA 120

Qy 3582 AAATCAGATATTGATTTAGTGTGTCGACAAAGACAACTGGTGTGCTTGCCAGGGCAATTTCTCAGAA 120

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Qy 3642 AATACAAAAAATCCGGAGAAATTTGCCCACTGCACCGCTGCTAACCATTTGCACACAG 3701

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Qy 3702 ATTGAACACCATTTATGACGCGACAGATATGTTTTAGATTTCAGGAAGACTGAAAGA 3761

Db 241 ATTGAACACCATTTATGACGCGACAGATATGTTTTAGATTTCAGGAAGACTGAAAGA 300

Qy 3762 ATATGATGAGCGGTATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTACAGATGGTGCA 3821

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Qy 3822 ACAACT 3827

Db 361 ACAACT 366

RESULT 3

LOCUS HSU83660

DEFINITION Human multidrug resistance-associated protein homolog (MRP4) mRNA, partial cds.

ACCESSION U83660

VERSION U83660.1 GI:2439971

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 486)

AUTHORS Kool, M., de Haas, M., Scheffer, G.L., Scheper, R.J., van Eijk, M.J., Juijn, J.A., Baas, F. and Borst, P.

TITLE Analysis of expression of cMOAT (MRP2), MRP3, MRP4, and MRP5, homologues of the multidrug resistance-associated protein gene (MRP1), in human cancer cell lines

JOURNAL Cancer Res. 57 (16), 3537-3547 (1997)

MEDLINE 97413640

PUBMED 9270026

REFERENCE 2 (bases 1 to 486)

AUTHORS Kool, M., de Haas, M., Pomme, N.J., Baas, F. and Borst, P.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-1997) Molecular Biology, Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands

FEATURES

source

1..486

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/translations="LKETIDLPKMDTELAGSNFSGVQROLVCLARAILRKNOIL IIDEANVDPRTDELIQKIRKFAHCTVLTIAHRLNTIIDSCKIWLDSGRUKEYD EPYVLQNKESLFYKVVQQLGKAEXXLTETAKXVYFKRNXHXIGDXHHVYNXNGX XS"

ORIGIN

Query Match 9.2%; Score 366; DB 9; Length 486;

Best Local Similarity 100.0%; Pred. No. 3.2e-196;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3462 ACTTAAAGAAACCATTTGAAGATCTTCTCGTAAATGATGACTCAATTTAGCAGATCAGG 3521

Db 1 ACTTAAAGAAACCATTTGAAGATCTTCTCGTAAATGATGACTCAATTTAGCAGATCAGG 60

Qy 3522 ATCCAAATTTAGTGTGTCGACAAAGACAACTGGTGTGCTTGCCAGGGCAATTTCTCAGAA 3581

Db 61 ATCCAAATTTAGTGTGTCGACAAAGACAACTGGTGTGCTTGCCAGGGCAATTTCTCAGAA 120

Qy 3582 AAATCAGATATTGATTTAGTGTGTCGACAAAGACAACTGGTGTGCTTGCCAGGGCAATTTCTCAGAA 120

Db 121 AAATCAGATATTGATTTAGTGTGTCGACAAAGACAACTGGTGTGCTTGCCAGGGCAATTTCTCAGAA 180

Qy 3642 AATACAAAAAATCCGGGAGAAATTTGCCACTGCAACCGTGTAAACATTGCACACAG 3701  
 Db 181 AATACAAAAAATCCGGGAGAAATTTGCCACTGCAACCGTGTAAACATTGCACACAG 240  
 Qy 3702 ATTGAACACCAATTATGACGCGCAAGATATGGTTTATGATTCAGGAAGACTGAAAGA 3761  
 Db 241 ATTGAACACCAATTATGACGCGCAAGATATGGTTTATGATTCAGGAAGACTGAAAGA 300  
 Qy 3762 ATATGATGAGCGGTATGTTTGGCTGCAAAATAAGAGAGCCCTATTTTACAAGATGGTGCA 3821  
 Db 301 ATATGATGAGCGGTATGTTTGGCTGCAAAATAAGAGAGCCCTATTTTACAAGATGGTGCA 360  
 Qy 3822 ACAACT 3827  
 Db 361 ACAACT 366  
 RESULT 4  
 LOCUS CQ508779 424 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 40646 from Patent WO0160860.  
 ACCESSION CQ508779  
 VERSION CQ508779.1 GI:41475043  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schlegel R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their use  
 JOURNAL Patent: WO 0160860-A 40646 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 424  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 8.4%; Score 336; DB 6; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-179;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 532 GCATTCGTCTTAGTAATGCGCATGGGGAAGAACCAACAGCCAGATAGTCAATCTG 591  
 Db 381 GCATTCGTCTTAGTAATGCGCATGGGGAAGAACCAACAGCCAGATAGTCAATCTG 322  
 Qy 592 CTGTCCCAATGATGAAACAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGGCA 651  
 Db 321 CTGTCCCAATGATGAAACAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGGCA 262  
 Qy 652 GGACCACTGCAGGCGATGCGAGTGCCTTCTCTGGATGAGATAGGAATATCGTGC 711  
 Db 261 GGACCACTGCAGGCGATGCGAGTGCCTTCTCTGGATGAGATAGGAATATCGTGC 202  
 Qy 712 CTTGCTGGATGGCAGTCTTAATCAATCTCTGCGCTTGGAAAGCTGTTTGGGAAGTTG 771  
 Db 201 CTTGCTGGATGGCAGTCTTAATCAATCTCTGCGCTTGGAAAGCTGTTTGGGAAGTTG 142  
 Qy 772 TTCTCATCACTGAGGATGAAACAGTCTTTCAGGATGCCAGATCAGGACCATGAT 831  
 Db 141 TTCTCATCACTGAGGATGAAACAGTCTTTCAGGATGCCAGATCAGGACCATGAT 82  
 Qy 832 GAAGTTAATCTGTTAAGGATATAAATAATGTAC 867  
 Db 81 GAAGTTAATCTGTTAAGGATATAAATAATGTAC 46

RESULT 5  
 LOCUS CQ508484

LOCUS CQ508484 407 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 40351 from Patent WO0160860.  
 ACCESSION CQ508484  
 VERSION CQ508484.1 GI:41474748  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schlegel R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their use  
 JOURNAL Patent: WO 0160860-A 40351 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 407  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 7.7%; Score 308; DB 6; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-163;  
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1955 GTACCTTCTCAGAGCTTCGGTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGATG 2014  
 Db 374 GTACCTTCTCAGAGCTTCGGTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGATG 315  
 Qy 2015 GTGCTCTGGAGAGCAAGATACAGAGATGTCACAGTTTACACTATCAGAGGAGAACCGTT 2074  
 Db 314 GTGCTCTGGAGAGCAAGATACAGAGATGTCACAGTTTACACTATCAGAGGAGAACCGTT 255  
 Qy 2075 CTGAAGAAAAGTTGGTTTTCAGGCCCTATAAGAAATTAATCTCAGAGCTGCTCACTGCA 2134  
 Db 254 CTGAAGAAAAGTTGGTTTTCAGGCCCTATAAGAAATTAATCTCAGAGCTGCTCACTGCA 195  
 Qy 2135 TTGCTTTCATTTCTTATCTTCTTAACTGCGAGCTCAGGTTGCTTCAAG 2194  
 Db 194 TTGCTTTCATTTCTTATCTTCTTAACTGCGAGCTCAGGTTGCTTCAAG 135  
 Qy 2195 ATTGGTGGCTTCTATCTATCTGGGCAACAAACAGATGCTAAATGTCTCTGTAATGGAG 2254  
 Db 134 ATTGGTGGCTTCTATCTATCTGGGCAACAAACAGATGCTAAATGTCTCTGTAATGGAG 75  
 Qy 2255 GAGGAAT 2262  
 Db 74 GAGGAAT 67  
 RESULT 6  
 LOCUS CQ492361 442 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 24228 from Patent WO0160860.  
 ACCESSION CQ492361  
 VERSION CQ492361.1 GI:41457980  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schlegel R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their use  
 JOURNAL Patent: WO 0160860-A 24228 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 442  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 7.1%; Score 283; DB 6; Length 442;  
Best Local Similarity 99.7%; Pred. No. 8.1e-149;  
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 532 GCACCTTCGTCTTAGTAACATGGCATGGGAAGACAAACCACAGCCAGATAGTCAATCTG 591  
Db 109 GCACCTTCGTCTTAGTAACATGGCATGGGAAGACAAACCACAGCCAGATAGTCAATCTG 168

Qy 592 CTGTCCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTCTTTACACTTCTCTGTGGGCA 651  
Db 169 CTGTCCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTCTTTACACTTCTCTGTGGGCA 228

Qy 652 GGACCACTGAGGGATGCGAGTGACATGCGCTTACTCTGTGATGGAGATAGGAATATCGTGC 711  
Db 229 GGACCACTGCGGGGATGCGAGTGACATGCGCTTACTCTGTGATGGAGATAGGAATATCGTGC 288

Qy 712 CTTGCTGGGATGGCAGTCTTAATCATTTCTCTGCGCTTGCAGAGCTGTTTGGGAAGTTG 771  
Db 289 CTTGCTGGGATGGCAGTCTTAATCATTTCTCTGCGCTTGCAGAGCTGTTTGGGAAGTTG 348

Qy 772 TTCTCATCACTGAGGATGAAACTGCAACTTTTCACGGATGCCAGATCAGGACCATGAAT 831  
Db 349 TTCTCATCACTGAGGATGAAACTGCAACTTTTCACGGATGCCAGATCAGGACCATGAAT 408

Qy 832 GAACTTATACTGTTATAGGATTAATAAATGT 865  
Db 409 GAACTTATACTGTTATAGGATTAATAAATGT 442

RESULT 7  
AR562517  
LOCUS AR562517 443 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 28 from patent US 6759238.  
ACCESSION AR562517  
VERSION AR562517.1 GI:53976592  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 443)  
AUTHORS Schuetz, J. and Fridland, A.  
TITLE Multidrug resistance associated proteins and uses thereof  
JOURNAL Patent: US 6759238-A 28 06-JUL-2004;  
FEATURES Location/Qualifiers  
source 1..443  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 6.5%; Score 260; DB 6; Length 443;  
Best Local Similarity 100.0%; Pred. No. 1.1e-135;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3719 ACAGCGACAAGATATGTTTATGATTCAGGAAGACTGAAAGATATGATGAGCGGTATG 3778  
Db 1 ACAGCGACAAGATATGTTTATGATTCAGGAAGACTGAAAGATATGATGAGCGGTATG 60

Qy 3779 TTTTGTGTCRAAATAAGAGAGCGCTATTATTACAGATGGTGCAACAACTGGGCAAGCGAG 3838  
Db 61 TTTTGTGTCRAAATAAGAGAGCGCTATTATTACAGATGGTGCAACAACTGGGCAAGCGAG 120

Qy 3839 AAGCGGCTGCCCTCACTGAAACAGCAACAGGATATCTTCAAAAGAAATATCCACATA 3898  
Db 121 AAGCGGCTGCCCTCACTGAAACAGCAACAGGATATCTTCAAAAGAAATATCCACATA 180

Qy 3899 TTGTCACACTGACCAATGATGTTTACAAACACTTCAATGGACAGCCCTCGACCTTAACATA 3958  
Db 181 TTGTCACACTGACCAATGATGTTTACAAACACTTCAATGGACAGCCCTCGACCTTAACATA 240

Qy 3959 TTTTCGAGACAGCACTGTGA 3978  
Db 1 TTTTCGAGACAGCACTGTGA 3978

Db 241 TTTTCGAGACAGCACTGTGA 260

RESULT 8  
CQ510062  
LOCUS CQ510062 425 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 41929 from Patent WO0160860.  
ACCESSION CQ510062  
VERSION CQ510062.1 GI:41476326  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
JOURNAL  
FEATURES Location/Qualifiers  
source 1..425  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 6.3%; Score 252; DB 6; Length 425;  
Best Local Similarity 100.0%; Pred. No. 4.1e-131;  
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 532 GCACCTTCGTCTTAGTAACATGGCATGGGAAGACAAACCACAGCCAGATAGTCAATCTG 591  
Db 174 GCACCTTCGTCTTAGTAACATGGCATGGGAAGACAAACCACAGCCAGATAGTCAATCTG 233

Qy 592 CTGTCCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTCTTTACACTTCTCTGTGGGCA 651  
Db 234 CTGTCCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTCTTTACACTTCTCTGTGGGCA 293

Qy 652 GGACCACTGAGGGATGCGAGTGACATGCGCTTACTCTGTGATGGAGATAGGAATATCGTGC 711  
Db 294 GGACCACTGAGGGATGCGAGTGACATGCGCTTACTCTGTGATGGAGATAGGAATATCGTGC 353

Qy 712 CTTGCTGGGATGGCAGTCTTAATCATTTCTCTGCGCTTGCAGAGCTGTTTGGGAAGTTG 771  
Db 354 CTTGCTGGGATGGCAGTCTTAATCATTTCTCTGCGCTTGCAGAGCTGTTTGGGAAGTTG 413

Qy 772 TTCTCATCACTG 783  
Db 414 TTCTCATCACTG 425

RESULT 9  
AX046491  
LOCUS AX046491 250 bp DNA linear PAT 24-NOV-2000  
DEFINITION Sequence 28 from Patent WO0058471.  
ACCESSION AX046491  
VERSION AX046491.1 GI:11344438  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Schuetz, J. and Fridland, A.  
TITLE Multidrug resistance associated proteins and uses thereof  
JOURNAL Patent: WO 0058471-A 28 05-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..250  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"



RESULT 11	AR405803	291 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 823 from patent US 6630305.				
DEFINITION	AR405803				
ACCESSION	AR405803				
VERSION	AR405803.1	GI:40154640			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 291)				
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.				
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer				
JOURNAL	Patent: US 6630305-A 823 07-OCT-2003;				
FEATURES	source	Location/Qualifiers			
	1..291	/organism="unknown"			
		/mol_type="genomic DNA"			
ORIGIN					
	Query Match	5.4%;	Score 216;	DB 6;	Length 291;
	Best Local Similarity	100.0%;	Pred. No. 1.5e-110;		
	Matches 216;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	3655	ATCCGGGAGAAATTTGCCCACTGCACCGTCTAAACCATTTGCACACAGATTGAACACCAT	3714		
Db	7	ATCCGGGAGAAATTTGCCCACTGCACCGTCTAAACCATTTGCACACAGATTGAACACCAT	66		
QY	3715	ATTGACAGCGACAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCG	3774		
Db	67	ATTGACAGCGACAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCG	126		
QY	3775	TATGTTTTCCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGTTGCAACAACCTGGGCAAG	3834		
Db	127	TATGTTTTCCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGTTGCAACAACCTGGGCAAG	186		
QY	3835	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG	3870		
Db	187	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG	222		
RESULT 12	AR564183	291 bp	DNA	linear	PAT 08-OCT-2004
LOCUS	Sequence 823 from patent US 6759515.				
DEFINITION	AR564183				
ACCESSION	AR564183				
VERSION	AR564183.1	GI:53979234			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 291)				
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.				
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer				
JOURNAL	Patent: US 6759515-A 823 06-JUL-2004;				
FEATURES	source	Location/Qualifiers			
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		/mol_type="genomic DNA"			
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	Best Local Similarity	100.0%;	Pred. No. 1.5e-110;		
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				Indels	0;
				Gaps	0;
QY	3655	ATCCGGGAGAAATTTGCCCACTGCACCGTCTAAACCATTTGCACACAGATTGAACACCAT	3714		
Db	7	ATCCGGGAGAAATTTGCCCACTGCACCGTCTAAACCATTTGCACACAGATTGAACACCAT	66		
QY	3715	ATTGACAGCGACAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCG	3774		
Db	67	ATTGACAGCGACAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCG	126		
QY	3775	TATGTTTTCCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGTTGCAACAACCTGGGCAAG	3834		
Db	127	TATGTTTTCCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGTTGCAACAACCTGGGCAAG	186		
QY	3835	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG	3870		
Db	187	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG	222		

ORIGIN	/note="Unknown"									
Query Match	6.3%;	Score 250;	DB 6;	Length 250;						
Best Local Similarity	100.0%;	Pred. No. 5.8e-130;								
Matches 250;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;						
Qy	3462	ACTTAAAGAAACCAATTGGAAGATCTTCTGTAATAATGGATAGTAAATAGCAAGATCAGG	3521							
Db	1	ACTTAAAGAAACCAATTGGAAGATCTTCTGTAATAATGGATAGTAAATAGCAAGATCAGG	60							
Qy	3522	ATCCAAATTTTAGTGTTCGACAAAGACAACACTGGTGTGCTTGCCTTGCACAGGCAATTTCTCAGGAA	3581							
Db	61	ATCCAAATTTTAGTGTTCGACAAAGACAACACTGGTGTGCTTGCCTTGCACAGGCAATTTCTCAGGAA	120							
Qy	3582	AAATCAGATATTGATTATTCATGAAGCGACGCGCAAAATGTGCGATCCAAAGAACTCATGAGTT	3641							
Db	121	AAATCAGATATTGATTATTCATGAAGCGACGCGCAAAATGTGCGATCCAAAGAACTCATGAGTT	180							
Qy	3642	AAATCAAAAAAATTCGGGAGAAATTTGCCCACTGCACCGTCTCAACCATTCACACAG	3701							
Db	181	AAATCAAAAAAATTCGGGAGAAATTTGCCCACTGCACCGTCTCAACCATTCACACAG	240							
Qy	3702	ATTGAACACC	3711							
Db	241	ATTGAACACC	250							
RESULT 10										
LOCUS	AR400536	291 bp	DNA	linear	PAT 18-DEC-2003					
DEFINITION	Sequence 823 from patent US 6620922.									
ACCESSION	AR400536									
VERSION	AR400536.1	GI:40144002								
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 291)									
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.									
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer									
JOURNAL	Patent: US 6620922-A	823 16-SEP-2003;								
FEATURES	Location/Qualifiers									
source	1..291	/organism="unknown"								
mol_type="genomic DNA"										
ORIGIN										
Query Match	5.4%;	Score 216;	DB 6;	Length 291;						
Best Local Similarity	100.0%;	Pred. No. 1.5e-110;								
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;						
Qy	3655	ATCCGGAGAAATTTGCCCACTGCACCGTCTCAACCATTCGACAGATTGAACACCAATT	3714							
Db	7	ATCCGGAGAAATTTGCCCACTGCACCGTCTCAACCATTCGACAGATTGAACACCAATT	66							
Qy	3715	ATTGACAGCACAAGATAATGGTTTATGATTCAGGAAGACTGAAAGAAATATGATGAGCCG	3774							
Db	67	ATTGACAGCACAAGATAATGGTTTATGATTCAGGAAGACTGAAAGAAATATGATGAGCCG	126							
Qy	3775	TATGTTTTCGCTCAAAATAAAGAGAGAGAGCTATTTTACAAAGATGTCGCAACAACTGGGCAAG	3834							
Db	127	TATGTTTTCGCTCAAAATAAAGAGAGAGAGCTATTTTACAAAGATGTCGCAACAACTGGGCAAG	186							
Qy	3835	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG	3870							
Db	187	GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG	222							
RESULT 11										
LOCUS	AR405803	291 bp	DNA	linear	PAT 18-DEC-2003					
DEFINITION	Sequence 823 from patent US 6630305.									
ACCESSION	AR405803									
VERSION	AR405803.1	GI:40154640								
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 291)									
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.									
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer									
JOURNAL	Patent: US 6630305-A	823 07-OCT-2003;								
FEATURES	Location/Qualifiers									
source	1..291	/organism="unknown"								
mol_type="genomic DNA"										
ORIGIN										
Query Match	5.4%;	Score 216;	DB 6;	Length 291;						

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Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCATTTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 3774
Db 67 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186

Qy 3835 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 3870
Db 187 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 222

RESULT 13
AX201050 291 bp DNA linear PAT 29-AUG-2001
LOCUS
DEFINITION Sequence 680 from Patent WO0151633.
ACCESSION AX201050
VERSION AX201050.1 GI:15390858
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 680 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..291
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 5.4%; Score 216; DB 6; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCATTTGCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCATTTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 3774
Db 67 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186

Qy 3835 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 3870
Db 187 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 222

RESULT 14
AX267849 291 bp DNA linear PAT 26-OCT-2001
LOCUS
DEFINITION Sequence 823 from Patent WO0173032.
ACCESSION AX267849
VERSION AX267849.1 GI:16516495
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
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REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hegler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 823 04-OCT-2001;
CORIXA CORPORATION (US)
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Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCATTTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 3774
Db 67 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186

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ACCESSION BD076840
VERSION BD076840.1 GI:22622443
KEYWORDS JP 2001512013-A/87.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of secretory protein expressed in prostate
JOURNAL Patent: JP 2001512013-A 87 21-AUG-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001512013-A/87
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
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Copyright (c) 1993 - 2005 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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6	216	5.4	291	9	US-09-780-669-823
7	216	5.4	291	9	US-09-822-827-823
8	216	5.4	291	9	US-09-895-793-823
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## ALIGNMENTS

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; Sequence 40646, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endegge, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
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; Sequence 41929, Application US/10357930

; Publication No. US20040259086A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Endege, Wilson

; APPLICANT: Monahan, John

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

; TITLE OF INVENTION: HUMAN PROSTATE CANCER

; FILE REFERENCE: MRI-007BCN

; CURRENT APPLICATION NUMBER: US/10/357,930

; CURRENT FILING DATE: 2003-02-04

; PRIOR APPLICATION NUMBER: 09/785,276

; PRIOR FILING DATE: 2003-02-16

; PRIOR APPLICATION NUMBER: 60/183,319

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 60/189,862

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; Sequence 823, Application US/09759143

; Patent No. US20020022248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

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; TYPE: DNA

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Db 7 ATCCGGGAGAAATTTGCCCACTGCGCTGCTAACACCTGACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGACACAGATTAATGGTTTATAGATTCAGGAAGACTGAAAGATATATGATGAGCG 3774

Db 67 ATTGACAGCGACACAGATTAATGGTTTATAGATTCAGGAAGACTGAAAGATATATGATGAGCG 126

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US-09-780-669-823

; Sequence 823, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

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; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
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US-09-822-827-823
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; Sequence 823, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
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; ORGANISM: Homo sapiens
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Db 187 GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAACAG 222

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; Sequence 823, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
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; ORGANISM: Homo sapiens
US-09-895-793-823

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAGAAATTTGCCACTGACCGTGTAAACCACTTGCACACAGATTGAACACCACTT 3714
Db 7 ATCCGGAGAGAAATTTGCCACTGACCGTGTAAACCACTTGCACACAGATTGAACACCACTT 66

Qy 3715 ATTGACAGCGACGATTAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGACGATTAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 126

Qy 3775 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGCAAG 3834
Db 127 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGCAAG 186

Qy 3835 GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAACAG 222
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Db 67 ATTGACAGCGACGATTAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 126
Qy 3775 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGCAAG 3834
Db 127 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGCAAG 186
Qy 3835 GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAACAG 222

RESULT 8
US-09-895-793-823
; Sequence 823, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-823

Query Match
Best Local Similarity 100.0%; Score 216; DB 9; Length 291;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAGAAATTTGCCACTGACCGTGTAAACCACTTGCACACAGATTGAACACCACTT 3714
Db 7 ATCCGGAGAGAAATTTGCCACTGACCGTGTAAACCACTTGCACACAGATTGAACACCACTT 66

Qy 3715 ATTGACAGCGACGATTAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGACGATTAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 126

Qy 3775 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGCAAG 3834
Db 127 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCACAACTGGGCAAG 186

Qy 3835 GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAACAG 222
```



```
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144.678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-823

Query Match      5.4%; Score 216; DB 16; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTGGCCACTGCACCGTGTACACCTTGCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTGGCCACTGCACCGTGTACACCTTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGCAAGATAAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGCAAGATAAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 126

Qy 3775 TATGTTTCTGCGAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAG 3834
Db 127 TATGTTTCTGCGAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAG 186

Qy 3835 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 222

RESULT 12
US-10-294-025-823
; Sequence 823, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294.025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-823

Query Match      5.4%; Score 216; DB 16; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTGGCCACTGCACCGTGTACACCTTGCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTGGCCACTGCACCGTGTACACCTTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGCAAGATAAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGCAAGATAAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 126
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Qy 3775 TATGTTTCTGCGAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAG 3834
Db 127 TATGTTTCTGCGAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAG 186

Qy 3835 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 222

RESULT 13
US-10-357-930-41689
; Sequence 41689, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357.930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41689
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-41689

Query Match      5.3%; Score 210; DB 18; Length 391;
Best Local Similarity 100.0%; Pred. No. 2.5e-101;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 532 GCACCTTCGTCTTAGTAACATGGCCATGGGAAGACAACCAAGCAGCCAGATAGTCAATCTG 591
Db 167 GCACCTTCGTCTTAGTAACATGGCCATGGGAAGACAACCAAGCAGCCAGATAGTCAATCTG 226

Qy 592 CTGTCCAATGATGTGAACAAGTTTGATCAGGTGACGTGTTCTTACACTTCTCTGTGGGCA 651
Db 227 CTGTCCAATGATGTGAACAAGTTTGATCAGGTGACGTGTTCTTACACTTCTCTGTGGGCA 286

Qy 652 GGACCACTGCAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGC 711
Db 287 GGACCACTGCAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGC 346

Qy 712 CTGTCTGGGATGGCAGTTCTTAATCAATTCTC 741
Db 347 CTGTCTGGGATGGCAGTTCTTAATCAATTCTC 376

RESULT 14
US-10-930-32647
; Sequence 32647, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
```

```

; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32647
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-32647

Query Match      5.2%; Score 208; DB 18; Length 444;
Best Local Similarity 100.0%; Pred. No. 3e-100;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 568 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 627
Db 225 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 284

Qy 628 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 687
Db 285 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 344

Qy 688 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCATTAATCATTTCTCTGCCCC 747
Db 345 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCATTAATCATTTCTCTGCCCC 404

Qy 748 TTGCAAGCTGTTTGGGAAGTTGTTCT 775
Db 405 TTGCAAGCTGTTTGGGAAGTTGTTCT 432

RESULT 15
US-10-357-930-11475
; Sequence 11475, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25

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; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11475
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-11475

Query Match      5.2%; Score 208; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 3e-100;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 568 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 627
Db 180 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 239

Qy 628 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 687
Db 240 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 299

Qy 688 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCATTAATCATTTCTCTGCCCC 747
Db 300 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCATTAATCATTTCTCTGCCCC 359

Qy 748 TTGCAAGCTGTTTGGGAAGTTGTTCT 775
Db 360 TTGCAAGCTGTTTGGGAAGTTGTTCT 387

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Job time : 2180 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 18:21:20 ; Search time 12058 Seconds  
(without alignments)  
12557.610 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcgcgtgtaccagga.....ttttcgagacagcactgtga 3978

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 29252628

Minimum DB seq length: 0

Maximum DB seq length: 500

Post-processing: Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gss1.\*
- 9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491	12.3	491	5 BX474791	BX474791 DKFZp686G
2	472	11.9	497	1 AL701816	AL701816 DKFZp686F
3	435	10.9	435	2 BE327296	BE327296 hw10b05.x
4	406	10.2	465	1 AUI26646	AUI26646 AUI26646
5	361	9.1	478	2 BE674208	BE674208 7d76g07.x
6	341	8.6	447	7 CN410193	CN410193 170005321
7	294	7.4	383	7 R35797	R35797 YG66a11.r1
8	234	5.9	367	1 AA305627	AA305627 EST176623
9	198	5.0	367	2 BE769452	BE769452 QV3-FT003
10	178	4.5	348	2 BE838702	BE838702 RC6-FN011
11	178	4.5	405	2 BE838708	BE838708 RC6-FN011
12	178	4.5	413	2 BE838700	BE838700 RC6-FN011
13	178	4.5	443	2 BE838704	BE838704 RC6-FN011
14	177	4.4	415	2 BE838703	BE838703 RC6-FN011
15	175	4.4	377	2 BE838720	BE838720 RC6-FN011
16	149	3.7	254	2 BE769429	BE769429 PM4-FT002
17	145	3.6	405	2 BE838733	BE838733 RC6-FN011
18	145	3.6	482	7 R00050	R00050 YG70605.s1
19	137	3.4	290	1 AA375392	AA375392 EST87662
20	132	3.3	344	2 BE838696	BE838696 RC6-FN011
21	131	3.3	411	2 BE838692	BE838692 RC6-FN011
22	128	3.2	179	2 BE765041	BE765041 IL2-NT009
23	117	2.9	252	8 CC325199	CC325199 XL153 Bay
24	113	2.8	329	2 BE838725	BE838725 RC6-FN011

c	25	110	2.8	326	2	BE769242	BE769242	PM4-FT002
	26	99	2.5	310	2	BF360747	BF360747	QV2-OT006
	27	97	2.4	357	8	AQ088953	AQ088953	HS_3004 B
	28	74	1.9	124	2	BE153864	BE153864	PM0-HT033
	29	72	1.8	190	2	BE174699	BE174699	QV2-HT057
	30	59	1.5	133	1	AI569098	AI569098	tr82a09.x
	31	53	1.3	351	2	BE838707	BE838707	RC6-FN011
	32	50	1.3	336	8	AQ088957	AQ088957	HS_3004 B
	33	41	1.0	418	1	AJ683278	AJ683278	AJ683278
	34	39	1.0	415	2	BF836367	BF836367	RC3-HT023
	35	38	1.0	132	9	CG869157	CG869157	AC0303 Sa
	36	38	1.0	175	9	CC894135	CC894135	RRK160 Ba
	37	38	1.0	362	7	CK337853	CK337853	C0347H04
	38	38	1.0	406	4	BI403742	BI403742	MI-P-CF1-
	39	36	0.9	487	2	BF231451	BF231451	253864 BA
	40	35	0.9	264	2	BE838685	BE838685	RC6-FN011
	41	35	0.9	465	4	BI540773	BI540773	454162 MA
	42	33	0.8	157	2	BE769293	BE769293	PM4-FT002
	43	33	0.8	380	4	BI044374	BI044374	PM4-OT021
	44	33	0.8	469	7	CN677720	CN677720	E0101B09-
	45	32	0.8	453	4	BM287170	BM287170	527468 MA

ALIGNMENTS

RESULT 1  
BX474791  
LOCUS BX474791 491 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp686G03172\_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone  
DKFZp686G03172 5', mRNA sequence.  
ACCESSION BX474791  
VERSION BX474791.1 GI:31668993  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 491)  
AUTHORS Bloembergen, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobos, G., Han, M. and Wiemann, S.  
EST (Bloembergen, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686G03172) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686G03172"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
/note="vector: pTriplex2; Site\_1: SfIIA; Site\_2: SfiIB; CDNA-collection"

ORIGIN

Query Match 12.3%; Score 491; DB 5; Length 491;  
Best Local Similarity 100.0%; Pred. No. 7e-257;  
Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1906 GAGGAAAGTGAACACCTCCAGTTCACGAACTCCCACTAAGGAATCGTACCTTCTCA 1965
Db 1 GAGGAAAGTGAACACCTCCAGTTCACGAACTCCCACTAAGGAATCGTACCTTCTCA 60

Qy 1966 GAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGAAGTGGTCTCTGGAG 2025
Db 61 GAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGAAGTGGTCTCTGGAG 120

Qy 2026 AGCCAAGATACAGAGAATGTCACAGTTCACATATCAGAGGAGAACCCGTTCTGAAGGAAA 2085
Db 121 AGCCAAGATACAGAGAATGTCACAGTTCACATATCAGAGGAGAACCCGTTCTGAAGGAAA 180

Qy 2086 GTTGGTTTTCAGGCTTAAGAAATTAATCTTACAGAGCTGGTCTCACTGGATTGCTTCATT 2145
Db 181 GTTGGTTTTCAGGCTTAAGAAATTAATCTTACAGAGCTGGTCTCACTGGATTGCTTCATT 240

Qy 2146 TTCCTTAATCTCCTAAACACTGCAGCTCAGGCTTCGCTATGCTTCAAGATTGGTGGCTT 2205
Db 241 TTCCTTAATCTCCTAAACACTGCAGCTCAGGCTTCGCTATGCTTCAAGATTGGTGGCTT 300

Qy 2206 TCATACGGGCAACAAACAAGTATGCTAAATGCTCACTGTAATGAGGAGGAAATGTA 2265
Db 301 TCATACGGGCAACAAACAAGTATGCTAAATGCTCACTGTAATGAGGAGGAAATGTA 360

Qy 2266 ACCGAGAGCTAGATCTTAACTGGTACTTACGAAATTTATTCAGGTTTAACTGTAGCTACC 2325
Db 361 ACCGAGAGCTAGATCTTAACTGGTACTTACGAAATTTATTCAGGTTTAACTGTAGCTACC 420

Qy 2326 GTTCTTTTGGCATAGCAAGATCTCTATTGGTATTTCTACGCTCTTGTGTTAACTCTTCAAA 2385
Db 421 GTTCTTTTGGCATAGCAAGATCTCTATTGGTATTTCTACGCTCTTGTGTTAACTCTTCAAA 480

Qy 2386 ACTTTGCACAA 2396
Db 481 ACTTTGCACAA 491

RESULT 2
AL701816 497 bp mRNA linear EST 04-SEP-2003
LOCUS DKFP686F08149_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFP686F08149 5', mRNA sequence.
ACCESSION AL701816
VERSION AL701816.1 GI:19685172
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFP686F08149) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1. 497
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686F08149"
/dev_stages="adult"
/lab_host="DH10B"
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ORIGIN
Query Match 11.9%; Score 472; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.9e-246;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1466 TGAGGAGTAATATTTTATTTGGGGAAGAAATACGAAAAGAACGATATGAAAAAGTCATAA 1525
Db 1 TGAGGAGTAATATTTTATTTGGGGAAGAAATACGAAAAGAACGATATGAAAAAGTCATAA 60

Qy 1526 AGCTTCTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGTGACTCTGCTGTGATAG 1585
Db 61 AGCTTCTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGTGACTCTGCTGTGATAG 120

Qy 1586 GAGATCGGGGAACCAACGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTCAAGAGAGCAG 1645
Db 121 GAGATCGGGGAACCAACGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTCAAGAGAGCAG 180

Qy 1646 TGTATCAAGATGCTGACATCTATCTCTGACAGATCCCTCAGTGCAGTAGATCGGGAAG 1705
Db 181 TGTATCAAGATGCTGACATCTATCTCTGACAGATCCCTCAGTGCAGTAGATCGGGAAG 240

Qy 1706 TTAGCAGACACTTGTTCGAACTGTGATTTGTCAAAATTTTGCATGAGAAGATCAAAATTT 1765
Db 241 TTAGCAGACACTTGTTCGAACTGTGATTTGTCAAAATTTTGCATGAGAAGATCAAAATTT 300

Qy 1766 TAGTGACTCATCAGTTGACGTACCTCAAAGTGCAGATCGAGATTTCTGATATTGAAAGATG 1825
Db 301 TAGTGACTCATCAGTTGACGTACCTCAAAGTGCAGATCGAGATTTCTGATATTGAAAGATG 360

Qy 1826 GTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGATATAGATTTTGGCT 1885
Db 361 GTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGATATAGATTTTGGCT 420

Qy 1886 CCCTTTTAAAGNAGGATAATCAGGAAAGTGAACAACCTCCAGTTCAGGAGAC 1937
Db 421 CCCTTTTAAAGNAGGATAATCAGGAAAGTGAACAACCTCCAGTTCAGGAGAAC 472

RESULT 3
BE327296/c 435 bp mRNA linear EST 14-JUL-2000
LOCUS hwi005.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182481 3'
DEFINITION similar to TR:075555 ABC TRANSPORTER MOAT-B ISOFORM ;, mRNA
sequence.
ACCESSION BE327296
VERSION BE327296.1 GI:9201072
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnlni.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 424.
Location/Qualifiers
FEATURES
```

source 1. 435  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3182481"  
 /tissue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Lu24"  
 /note="Organ: lung; Vector: pVT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 10.9%; Score 435; DB 2; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-226;  
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3211 GTTGGCATTGTGGAGAACCGGAGCTGGAAAGTTCCCTCATCTCAGCCCTTTTAGA 3270  
 Db 435 GTTGGCATTGTGGAGAACCGGAGCTGGAAAGTTCCCTCATCTCAGCCCTTTTAGA 376  
 Qy 3271 TTGTGACAGACCCGAGGTAAATTTGGATTGATAGATCTTGACAACTGAAATTTGGACTT 3330  
 Db 375 TTGTGACAGACCCGAGGTAAATTTGGATTGATAGATCTTGACAACTGAAATTTGGACTT 316  
 Qy 3331 CACGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTGTTCACCTGGAACA 3390  
 Db 315 CACGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTGTTCACCTGGAACA 256  
 Qy 3391 ATGAGGAAAACCTGGATCCCTTTAATGAGCAGACGGATGGAACCTGTGGAATGCCCTTA 3450  
 Db 255 ATGAGGAAAACCTGGATCCCTTTAATGAGCAGACGGATGGAACCTGTGGAATGCCCTTA 196  
 Qy 3451 CAAGAGGTACAACTTAAAGAAACCATTTAGATCTTCTGTTAAATGGATCTGAATTA 3510  
 Db 195 CAAGAGGTACAACTTAAAGAAACCATTTAGATCTTCTGTTAAATGGATCTGAATTA 136  
 Qy 3511 GCAGAAATCAGGATCCAAATTTTAGTGTGGACAAAGACAACTGTGTGCTTGCAGGGCA 3570  
 Db 135 GCAGAAATCAGGATCCAAATTTTAGTGTGGACAAAGACAACTGTGTGCTTGCAGGGCA 76  
 Qy 3571 ATTCTAGGAAAATCAGATATTGATTTAGTGAAGCGGCGCAATGTGGATCCAGA 3630  
 Db 75 ATTCTAGGAAAATCAGATATTGATTTAGTGAAGCGGCGCAATGTGGATCCAGA 16  
 Qy 3631 ACTGATCAGTTAATA 3645  
 Db 15 ACTGATCAGTTAATA 1

RESULT 4  
 LOCUS AUI26646 NT2RP1 Homo sapiens cdna clone NT2RP1001350 5', mRNA  
 DEFINITION sequence.  
 ACCESSION AUI26646  
 VERSION AUI26646.1 GI:10951362  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 465)  
 Oca.T., Nishikawa.T., Suzuki.Y., Kawai.Y., Ishii.S., Saito.K., Nakamura.Y., Nagai.T., Sugano.S. and Isogai.T.  
 HRI human cDNA project (Oca.T., Nishikawa.T., Suzuki.Y., Kawai.Y., Ishii.S., Saito.K., Nakamura.Y., Nagai.T., Sugano.S., Isogai.T.)

JOURNAL COMMENT

Unpublished (2000)  
 Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers

source 1. 465  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="NT2RP1001350"  
 /cell\_type="teratocarcinoma"  
 /note="Vector: pUC19FL3; mRNA from NT2 neuronal precursor cells after 48-hours retinoic acid (RA) induction"

ORIGIN

Query Match 10.2%; Score 406; DB 1; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-210;  
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3365 AGGAACTGTTTGTTCACCTGGAACAATGAGAAACCTGGATCCCTTTAATGAGCACA 3424  
 Db 14 AGGAACTGTTTGTTCACCTGGAACAATGAGAAACCTGGATCCCTTTAATGAGCACA 73  
 Qy 3425 CGGATGAGGAACCTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCACTGAAGATC 3484  
 Db 74 CGGATGAGGAACCTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCACTGAAGATC 133  
 Qy 3485 TTCTGTGTAATAGGATGATCTGAATTTAGCAGATCAGGATCCAAATTTTAGTGTGGACAAA 3544  
 Db 134 TTCTGTGTAATAGGATGATCTGAATTTAGCAGATCAGGATCCAAATTTTAGTGTGGACAAA 193  
 Qy 3545 GACAACTGTGTGCTTGCAGGCGCAATTTCTCAGGAAAATCAGATATTGATTTGATG 3604  
 Db 194 GACAACTGTGTGCTTGCAGGCGCAATTTCTCAGGAAAATCAGATATTGATTTGATG 253  
 Qy 3605 AAGCGACGCAAAATGTGATCCCAAGAACTGATGAGTTAATACAAAAAATCCGGGAGA 3664  
 Db 254 AAGCGACGCAAAATGTGATCCCAAGAACTGATGAGTTAATACAAAAAATCCGGGAGA 313  
 Qy 3665 AATTGCCCCACTGCACCGCTGCTAACCAATTGCACACAGATTGCAACCAATTTTACACGCG 3724  
 Db 314 AATTGCCCCACTGCACCGCTGCTAACCAATTGCACACAGATTGCAACCAATTTTACACGCG 373  
 Qy 3725 ACAAGATAATGTTTGTAGATTCAGGAAGACTGAAAGAATATGATGA 3770  
 Db 374 ACAAGATAATGTTTGTAGATTCAGGAAGACTGAAAGAATATGATGA 419

RESULT 5  
 LOCUS BE674208/c  
 DEFINITION "7d76g07.x1 NCI CGAP Lu24 Homo sapiens cdna clone IMAGE:3278940 3', similar to TR:075555 075555 ABC TRANSPORTER MOAT-B ISOFORM ;, mRNA sequence.  
 ACCESSION BE674208.1 GI:10034749  
 VERSION BE674208  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 478)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 446.  
FEATURES  
source  
1. .478  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3278940"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lu24"  
/note="Organ: lung; Vector: p77T3D-Pac (Pharmacia) with a  
modified polylinker; Plasmid DNA from the normalized  
library NCI CGAP Lu5 was prepared, and ss circles were  
made in vitro. Following HAP purification, this DNA was  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (cloneIDs  
141920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 9.1%; Score 361; DB 2; Length 478;  
Best Local Similarity 100.0%; Pred. No. 1.6e-185;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3283 GAAGTAAATTTGGATTGATAAGATCTTGACAACTGAAATGGACTTCACGATTTAAGG 3342  
Db 367 GAAGTAAATTTGGATTGATAAGATCTTGACAACTGAAATGGACTTCACGATTTAAGG 308  
Qy 3343 AAGAAATGTAATCATACCTCAGAACCTGTTTGTTCATCTGGAACAAATGAGGAAAAAC 3402  
Db 307 AAGAAATGTAATCATACCTCAGAACCTGTTTGTTCATCTGGAACAAATGAGGAAAAAC 248  
Qy 3403 CTGGATCCCTTTAATGACACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAA 3462  
Db 247 CTGGATCCCTTTAATGACACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAA 188  
Qy 3463 CTTAAGAAACCAATTGAAGATCTTCTCGTGAATGGAATCTGAATAGCAGATCAGGA 3522  
Db 187 CTTAAGAAACCAATTGAAGATCTTCTCGTGAATGGAATCTGAATAGCAGATCAGGA 128  
Qy 3523 TCCAAATTTAGTTGGCAAGACAACTGTGTGCTTGTCCAGGCGCAATCTCAGGAAA 3582  
Db 127 TCCAAATTTAGTTGGCAAGACAACTGTGTGCTTGTCCAGGCGCAATCTCAGGAAA 68  
Qy 3583 AATCAGATATTGATTATTGATGAACGCGCAATGTTGGAATCCAAAGAACTGATGAGTTA 3642  
Db 67 AATCAGATATTGATTATTGATGAACGCGCAATGTTGGAATCCAAAGAACTGATGAGTTA 8  
Qy 3643 A 3643  
Db 7 A 7

RESULT 6  
CN410193  
LOCUS CN410193 447 bp mRNA linear EST 16-MAY-2004  
DEFINITION 17000532183702 GRN\_ES Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN410193

CN410193.1 GI:47397317

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 447)

REFERENCE

AUTHORS

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.

TITLE

Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation

JOURNAL

COMMENT

Nat. Biotechnol. 22 (6): 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert length: 447 Std Error: 0.00.

FEATURES

source

1. .447  
Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="embryonic stem cells, cell lines H1, H7, and  
H9"

/clone\_lib="GRN ES"

/note="oligo dT primed, full-length enriched cDNA library  
from undifferentiated hES cell lines H1 (p32), H7 (p29),  
and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 8.6%; Score 341; DB 7; Length 447;

Best Local Similarity 99.7%; Pred. No. 1.5e-174;

Matches 391; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 559 GGGGAAGACACACAGCCAGATAGTCAATCTGCTGCCAATGATGTGAACAAGTTTGAT 618

Db 1 GGGGAAGACACACAGCCAGATAGTCAATCTGCTGCCAATGATGTGAACAAGTTTGAT 60

Qy 619 CAGGTGACAGTGTCTTACACTTCCTGTGGCAGACCACTGCAGGCGATCGCAGTGACT 678

Db 61 CAGGTGACAGTGTCTTACACTTCCTGTGGCAGACCACTGCAGGCGATCGCAGTGACT 120

Qy 679 GCCCTACTCTGGATGGAGATAGGAATATCGTCCTCTGGATGGCAGTTCTAATCATT 738

Db 121 GCCCTACTCTGGATGGAGATAGGAATATCGTCCTCTGGATGGCAGTTCTAATCATT 180

Qy 739 CTCCTGCCCTTGCAAAAGCTGTTTGGGAAGTGTGTTCTCATCCTGAGGAGTAAACTGCA 798

Db 181 CTCCTGCCCTTGCAAAAGCTGTTTGGGAAGTGTGTTCTCATCCTGAGGAGTAAACTGCA 240

Qy 799 ACTTTCACGGATGCCAGGATCAGACCACTGAATGAAGTTAATCTGTTAAGCATATA 858

Db 241 ACTTTCACGGATGCCAGGATCAGACCACTGAATGAAGTTAATCTGTTAAGCATATA 300

Qy 859 AAAATGTACGCTGGGAAAAGTCATTTCAAATCTTATTACCAATTTGAGAAAGAGAG 918

Db 301 AAAATGTACGCTGGGAAAAGTCATTTCAAATCTTATTACCAATTTGAGAAAGAGAG 360

Qy 919 ATTTCCAAAGATCTGAGAAGTTCTCCTGCTCAG 950

Db 361 ATTTCCAAAGATCTGAGAAGTTCTCCTGCTCAG 392

RESULT 7

R35797

LOCUS

DEFINITION

R35797 383 bp mRNA linear EST 02-MAY-1995  
Y966a11.f1 Soares infant brain INIB Homo sapiens cDNA clone  
IMAGE:38089 5', similar to SP:MRP HUMAN P33527 MULTIDRUG  
RESISTANCE-ASSOCIATED ;, mRNA sequence.

[illegible]





application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 4.5%; Score 178; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-85;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2918 CTCCTGGATGCGGCGAGGTTGGTTGGCAGCTGCTATGCGCCTCACGCTCATGGGATGT 2977  
 Db 222 CTCCTGGATGCGGCGAGGTTGGTTGGCAGCTGCTATGCGCCTCACGCTCATGGGATGT 163  
 Qy 2978 TTCAGTGGTGTGTTTCGACAAAGTCTGAAAGTTGAGAATATGATGATCTCAGTAGAAGGG 3037  
 Db 162 TTCAGTGGTGTGTTTCGACAAAGTCTGAAAGTTGAGAATATGATGATCTCAGTAGAAGGG 103  
 Qy 3038 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 3095  
 Db 102 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 45

RESULT 11

BE838708/c

LOCUS BE838708 405 bp mRNA linear EST 22-SEP-2000

DEFINITION RC6-FN0112-190700-011-E02 FN0112 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE838708

VERSION BE838708.1 GI:10271086

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 405)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-FN0112-190

700-011-E02&t3=2000-07-19&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 27

High quality sequence stop: 404.

Location/Qualifiers

1. 405

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="FN0112"

/note="Organ: prostate normal; Vector: puc18; Site 1:

SmaI; Site 2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 4.5%; Score 178; DB 2; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-85;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2918 CTCCTGGATGCGGCGAGGTTGGTTGGCAGCTGCTATGCGCCTCACGCTCATGGGATGT 2977  
 Db 227 CTCCTGGATGCGGCGAGGTTGGTTGGCAGCTGCTATGCGCCTCACGCTCATGGGATGT 168  
 Qy 2978 TTCAGTGGTGTGTTTCGACAAAGTCTGAAAGTTGAGAATATGATGATCTCAGTAGAAGGG 3037  
 Db 167 TTCAGTGGTGTGTTTCGACAAAGTCTGAAAGTTGAGAATATGATGATCTCAGTAGAAGGG 108  
 Qy 3038 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 3095  
 Db 107 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 50

RESULT 12

BE838700/c

LOCUS BE838700 413 bp mRNA linear EST 22-SEP-2000

DEFINITION RC6-FN0112-190700-011-B03 FN0112 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE838700

VERSION BE838700.1 GI:10271078

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-FN0112-190

700-011-B03&t3=2000-07-19&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 382.

Location/Qualifiers

1. 413

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="FN0112"

/note="Organ: prostate normal; Vector: puc18; Site 1:

SmaI; Site 2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

```

ORIGIN
Query Match      4.5%; Score 178; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2918 CTCGTGGATGCGGCGCAGTGGTTGGTTCGACATGCTCTATGCTCCTATGCCCTCACGCTCATGGGGATGT 2977
Db 217 CTCGTGGATGCGGCGCAGTGGTTGGTTCGACATGCTCTATGCTCCTATGCCCTCACGCTCATGGGGATGT 158
Qy 2978 TTCAGTGGTGTGTTTCGACAAAGTCTCGAAGTTGAGAAATATGATGATCTTCAGTAGAAAAGGG 3037
Db 157 TTCAGTGGTGTGTTTCGACAAAGTCTCGAAGTTGAGAAATATGATGATCTTCAGTAGAAAAGGG 98
Qy 3038 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTCGGGAATATCAGAAAGCGCCACC 3095
Db 97 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTCGGGAATATCAGAAAGCGCCACC 40

RESULT 13
BE838704/c
LOCUS BE838704 443 bp mRNA linear EST 22-SEP-2000
DEFINITION RC6-FN0112-190700-011-C04 FN0112 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE838704
VERSION BE838704.1 GI:10271082
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 443)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=st2=RC6-FN0112-190700-011-C04&t3=2000-07-19&t4=1)
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1. 443
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/note="Organ: prostate normal; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match      4.4%; Score 177; DB 2; Length 415;
Best Local Similarity 99.6%; Pred. No. 1.6e-84;

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Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 220 CTCGTGGATGCGGCGCAGTGGTTGGTTCGACATGCTCTATGCTCCTATGCCCTCACGCTCATGGGGATGT 161
Qy 2978 TTCAGTGGTGTGTTTCGACAAAGTCTCGAAGTTGAGAAATATGATGATCTTCAGTAGAAAAGGG 3037
Db 160 TTCAGTGGTGTGTTTCGACAAAGTCTCGAAGTTGAGAAATATGATGATCTTCAGTAGAAAAGGG 101
Qy 3038 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTCGGGAATATCAGAAAGCGCCACC 3095
Db 100 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTCGGGAATATCAGAAAGCGCCACC 43

RESULT 14
BF836367/c
LOCUS BF836367 415 bp mRNA linear EST 13-JAN-2001
DEFINITION RC3-HT0230-171100-117-e08 HT0230 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF836367
VERSION BF836367.1 GI:12188188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 415)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC3&t2=RC3-HT0230-171100-117-e08&t3=2000-11-17&t4=1)
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High quality sequence start: 41
High quality sequence stop: 415.
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/note="Organ: head neck; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match      4.4%; Score 177; DB 2; Length 415;
Best Local Similarity 99.6%; Pred. No. 1.6e-84;

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Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3332 ACGATTTAAGGAAGAAATGCAATCATACCTCAGGAACCTGTTTGTTCACCTGGAACAA 3391

Db 378 ACGATTTAAGGAAGAAATGCAATCATACCTCAGGAACCTGTTTGTTCACCTGGAACAA 319

Qy 3392 TGAGGAAAAACCTGGATCCCTTTAATGAGCACGAGATGAGGAACCTGTGGAATCCCTTAC 3451

Db 318 TGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGGTGAGGAACCTGTGGAATCCCTTAC 259

Qy 3452 AAGAGGTACAACTTAAAGAACCACTTGAAGATCTTCTGGTAAATCGATCTCAATTAG 3511

Db 258 AAGAGGTACAACTTAAAGAACCACTTGAAGATCTTCTGGTAAATCGATCTCAATTAG 199

Qy 3512 CAGAATCAGGATCCAAATTTTAGTGTGGACAAACCACTGTGTGCC 3559

Db 198 CAGNATCAGGATCCAAATTTTAGTGTGGACAAACCACTGTGTGCC 151

RESULT 15

BE838720/c

LOCUS BE838720 377 bp mRNA linear EST 22-SEP-2000

DEFINITION RC6-FN0112-190700-021-E06 FN0112 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE838720

VERSION BE838720.1 GI:10271098

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 377)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

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Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC6-FN0112-190700-021-E06&t3=2000-07-19&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 71

High quality sequence stop: 248.

Location/Qualifiers

FEATURES

1. .377

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/dev\_stage="Adult"

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ORIGIN

Query Match 4.4%; Score 175; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 2e-83;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 239 CTCTGGATGCGGSCAGGTTGGTTTGGCAGCTGTCTATGCCTCACGCTCATGGGATGT 180

Qy 2978 TTCAGTGGTGTGTTTCGACAAAGTCTCGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGG 3037

Db 179 TTCAGTGGTGTGTTTCGACAAAGTCTCGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGG 120

Qy 3038 TCATTGAATACACAGACCTTGAAGAAAGACGACCTTGGGAATATCAGAAACGCC 3092

Db 119 TCATTGAATACACAGACCTTGAAGAAAGACGACCTTGGGAATATCAGAAACGCC 65

Search completed: May 20, 2005, 03:10:27

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